

I hereby certify that, on the date shown below, this correspondence is being:

- ☒ deposited with the United States Postal Service in an envelope addressed to:
ASSISTANT COMMISSIONER FOR PATENTS, WASHINGTON, D.C. 20231,
☐ under 37CFR § 1.8(a), with sufficient postage as first class mail, or
☒ under 37CFR § 1.10, as "Express Mail Post Office to Addressee" Mailing Label No.
EL 367 647 761 US,
☐ transmitted by facsimile to the Patent and Trademark Office, Fax Number _____,
Attention: Examiner _____, Art Unit 16xx

PATENT

Attorney Docket No.
DX0724XK1

CN 028008

Date: September 10, 2001 By: _____

Jeffrey Gillis
Jeffrey Gillis

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Gerard T. HARDIMAN, et al.

Serial No.: to be assigned

Filed: SEPTEMBER 10, 2001

For: HUMAN RECEPTOR PROTEINS;
RELATED REAGENTS AND
METHODS

Examiner: not assigned

Art Unit: not assigned

USE OF PRIOR SEQUENCE
SUBMISSION UNDER 37 CFR §1.821(e)

Palo Alto, California 94304

SEPTEMBER 10, 2001

Assistant Commissioner for Patents
Box: Patent Application
Washington, D.C. 20231

Sir:

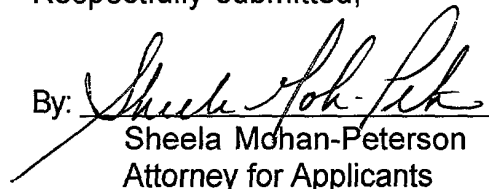
The attached copy of the Sequence Submission is for the patent application submitted herewith. The computer readable form in this application is equivalent to with that filed in parent application USSN 09/728,540. In accordance with 37 CFR 1.821(e), please use the computer readable form submitted in that application on July 17, 2001, as the computer readable form for the instant application. It is understood that the Patent and Trademark Office will make the necessary changes in application number and filing date for computer readable form that will be used for the instant application.

The attached copy of the Sequence Submission was originally submitted to the patent office in the parent application, USSN 09/728,540, in response to the Notice to Comply with Requirements for Patent Applications containing Nucleotide and/or Amino Acid Sequences dated June 7, 2001, for incorporation into the specification, on July 17, 2001.

Respectfully submitted,

Dated: September 10, 2001

By:


Sheela Mohan-Peterson
Attorney for Applicants
Reg. No. 41,201

DNAX Research Institute
901 California Avenue
Palo Alto, California 94304-1104
Tel: (650) 496-6400
Fax: (650) 496-1200

SEQUENCE LISTING

<110> Hardiman, Gerard T.
 Rock, Fernando L.
 Bazan, J. Fernando
 Kastelein, Robert A.
 Ho, Stephen W.K.
 Liu, Yong-Jun

<120> Human Receptor Proteins; Related Reagents and Methods

<130> DX0724XK

<140> 09/728,540

<141> 2000-11-28

<160> 45

<170> PatentIn Ver. 2.0

<210> 1

<211> 2367

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>

<221> CDS

<222> (1)..(2358)

<220>

<221> mat_peptide

<222> (67)..(2358)

<400> 1

atg	act	agc	atc	ttc	cat	ttt	gcc	att	atc	ttc	atg	tta	ata	ctt	cag	48
Met	Thr	Ser	Ile	Phe	His	Phe	Ala	Ile	Ile	Phe	Met	Leu	Ile	Leu	Gln	
		-20					-15					-10				

atc	aga	ata	caa	tta	tct	gaa	gaa	agt	gaa	ttt	tta	gtt	gat	agg	tca	96
Ile	Arg	Ile	Gln	Leu	Ser	Glu	Glu	Ser	Glu	Phe	Leu	Val	Asp	Arg	Ser	
	-5				-1	1				5					10	

aaa	aac	ggt	ctc	atc	cac	gtt	cct	aaa	gac	cta	tcc	cag	aaa	aca	aca	144
Lys	Asn	Gly	Leu	Ile	His	Val	Pro	Lys	Asp	Leu	Ser	Gln	Lys	Thr	Thr	
			15						20					25		

atc	tta	aat	ata	tcg	caa	aat	tat	ata	tct	gag	ctt	tgg	act	tct	gac	192
Ile	Leu	Asn	Ile	Ser	Gln	Asn	Tyr	Ile	Ser	Glu	Leu	Trp	Thr	Ser	Asp	
			30						35						40	

atc	tta	tca	ctg	tca	aaa	ctg	agg	att	ttg	ata	att	tct	cat	aat	aga	240
Ile	Leu	Ser	Leu	Ser	Lys	Leu	Arg	Ile	Leu	Ile	Ile	Ser	His	Asn	Arg	
	45						50					55				
atc	cag	tat	ctt	gat	atc	agt	gtt	ttc	aaa	ttc	aac	cag	gaa	ttg	gaa	288
Ile	Gln	Tyr	Leu	Asp	Ile	Ser	Val	Phe	Lys	Phe	Asn	Gln	Glu	Leu	Glu	
	60					65					70					
tac	ttg	gat	ttg	tcc	cac	aac	aag	ttg	gtg	aag	att	tct	tgc	cac	cct	336
Tyr	Leu	Asp	Leu	Ser	His	Asn	Lys	Leu	Val	Lys	Ile	Ser	Cys	His	Pro	
	75				80					85					90	
act	gtg	aac	ctc	aag	cac	ttg	gac	ctg	tca	ttt	aat	gca	ttt	gat	gcc	384
Thr	Val	Asn	Leu	Lys	His	Leu	Asp	Leu	Ser	Phe	Asn	Ala	Phe	Asp	Ala	
				95				100						105		
ctg	cct	ata	tgc	aaa	gag	ttt	ggc	aat	atg	tct	caa	cta	aaa	ttt	ctg	432
Leu	Pro	Ile	Cys	Lys	Glu	Phe	Gly	Asn	Met	Ser	Gln	Leu	Lys	Phe	Leu	
			110					115					120			
ggg	ttg	agc	acc	aca	cac	tta	gaa	aaa	tct	agt	gtg	ctg	cca	att	gct	480
Gly	Leu	Ser	Thr	Thr	His	Leu	Glu	Lys	Ser	Ser	Val	Leu	Pro	Ile	Ala	
		125					130					135				
cat	ttg	aat	atc	agc	aag	gtc	ttg	ctg	gtc	tta	gga	gag	act	tat	ggg	528
His	Leu	Asn	Ile	Ser	Lys	Val	Leu	Leu	Val	Leu	Gly	Glu	Thr	Tyr	Gly	
	140					145					150					
gaa	aaa	gaa	gac	cct	gag	ggc	ctt	caa	gac	ttt	aac	act	gag	agt	ctg	576
Glu	Lys	Glu	Asp	Pro	Glu	Gly	Leu	Gln	Asp	Phe	Asn	Thr	Glu	Ser	Leu	
	155				160					165					170	
cac	att	gtg	ttc	ccc	aca	aac	aaa	gaa	ttc	cat	ttt	att	ttg	gat	gtg	624
His	Ile	Val	Phe	Pro	Thr	Asn	Lys	Glu	Phe	His	Phe	Ile	Leu	Asp	Val	
				175					180					185		
tca	gtc	aag	act	gta	gca	aat	ctg	gaa	cta	tct	aat	atc	aaa	tgt	gtg	672
Ser	Val	Lys	Thr	Val	Ala	Asn	Leu	Glu	Leu	Ser	Asn	Ile	Lys	Cys	Val	
			190					195					200			
cta	gaa	gat	aac	aaa	tgt	tct	tac	ttc	cta	agt	att	ctg	gcg	aaa	ctt	720
Leu	Glu	Asp	Asn	Lys	Cys	Ser	Tyr	Phe	Leu	Ser	Ile	Leu	Ala	Lys	Leu	
		205					210					215				
caa	aca	aat	cca	aag	tta	tca	agt	ctt	acc	tta	aac	aac	att	gaa	aca	768
Gln	Thr	Asn	Pro	Lys	Leu	Ser	Ser	Leu	Thr	Leu	Asn	Asn	Ile	Glu	Thr	
	220					225					230					
act	tgg	aat	tct	ttc	att	agg	atc	ctc	caa	cta	gtt	tgg	cat	aca	act	816
Thr	Trp	Asn	Ser	Phe	Ile	Arg	Ile	Leu	Gln	Leu	Val	Trp	His	Thr	Thr	
	235				240					245					250	
gta	tgg	tat	ttc	tca	att	tca	aac	gtg	aag	cta	cag	ggg	cag	ctg	gac	864

Val	Trp	Tyr	Phe	Ser 255	Ile	Ser	Asn	Val	Lys 260	Leu	Gln	Gly	Gln	Leu 265	Asp	
ttc Phe	aga Arg	gat Asp	ttt Phe 270	gat Asp	tat Tyr	tct Ser	ggc Gly	act Thr 275	tcc Ser	ttg Leu	aag Lys	gcc Ala	ttg Leu 280	tct Ser	ata Ile	912
cac His	caa Gln	gtt Val 285	gtc Val	agc Ser	gat Asp	gtg Val	ttc Phe 290	ggg Gly	ttt Phe	ccg Pro	caa Gln	agt Ser 295	tat Tyr	atc Ile	tat Tyr	960
gaa Glu	atc Ile 300	ttt Phe	tcg Ser	aat Asn	atg Met	aac Asn 305	atc Ile	aaa Lys	aat Asn	ttc Phe	aca Thr 310	gtg Val	tct Ser	ggg Gly	aca Thr	1008
cgc Arg 315	atg Met	gtc Val	cac His	atg Met	ctt Leu 320	tgc Cys	cca Pro	tcc Ser	aaa Lys	att Ile 325	agc Ser	ccg Pro	ttc Phe	ctg Leu	cat His 330	1056
ttg Leu	gat Asp	ttt Phe	tcc Ser	aat Asn 335	aat Asn	ctc Leu	tta Leu	aca Thr	gac Asp 340	acg Thr	gtt Val	ttt Phe	gaa Glu	aat Asn 345	tgt Cys	1104
ggg Gly	cac His	ctt Leu	act Thr 350	gag Glu	ttg Leu	gag Glu	aca Thr	ctt Leu 355	att Ile	tta Leu	caa Gln	atg Met	aat Asn 360	caa Gln	tta Leu	1152
aaa Lys	gaa Glu	ctt Leu 365	tca Ser	aaa Lys	ata Ile	gct Ala	gaa Glu 370	atg Met	act Thr	aca Thr	cag Gln	atg Met 375	aag Lys	tct Ser	ctg Leu	1200
caa Gln	caa Gln	ttg Leu 380	gat Asp	att Ile	agc Ser	cag Gln 385	aat Asn	tct Ser	gta Val	agc Ser	tat Tyr 390	gat Asp	gaa Glu	aag Lys	aaa Lys	1248
gga Gly 395	gac Asp	tgt Cys	tct Ser	tgg Trp	act Thr 400	aaa Lys	agt Ser	tta Leu	tta Leu	agt Ser 405	tta Leu	aat Asn	atg Met	tct Ser	tca Ser 410	1296
aat Asn	ata Ile	ctt Leu	act Thr	gac Asp 415	act Thr	att Ile	ttc Phe	aga Arg	tgt Cys 420	tta Leu	cct Pro	ccc Pro	agg Arg	atc Ile 425	aag Lys	1344
gta Val	ctt Leu	gat Asp	ctt Leu 430	cac His	agc Ser	aat Asn	aaa Lys	ata Ile 435	aag Lys	agc Ser	att Ile	cct Pro	aaa Lys 440	caa Gln	gtc Val	1392
gta Val	aaa Lys	ctg Leu 445	gaa Glu	gct Ala	ttg Leu	caa Gln	gaa Glu 450	ctc Leu	aat Asn	gtt Val	gct Ala	ttc Phe 455	aat Asn	tct Ser	tta Leu	1440
act Thr	gac Asp 460	ctt Leu	cct Pro	gga Gly	tgt Cys	ggc Gly 465	agc Ser	ttt Phe	agc Ser	agc Ser	ctt Leu 470	tct Ser	gta Val	ttg Leu	atc Ile	1488

att	gat	cac	aat	tca	gtt	tcc	cac	cca	tca	gct	gat	ttc	ttc	cag	agc	1536
Ile	Asp	His	Asn	Ser	Val	Ser	His	Pro	Ser	Ala	Asp	Phe	Phe	Gln	Ser	
475					480					485					490	
tgc	cag	aag	atg	agg	tca	ata	aaa	gca	ggg	gac	aat	cca	ttc	caa	tgt	1584
Cys	Gln	Lys	Met	Arg	Ser	Ile	Lys	Ala	Gly	Asp	Asn	Pro	Phe	Gln	Cys	
				495					500					505		
acc	tgt	gag	ctc	gga	gaa	ttt	gtc	aaa	aat	ata	gac	caa	gta	tca	agt	1632
Thr	Cys	Glu	Leu	Gly	Glu	Phe	Val	Lys	Asn	Ile	Asp	Gln	Val	Ser	Ser	
			510					515					520			
gaa	gtg	tta	gag	ggc	tgg	cct	gat	tct	tat	aag	tgt	gac	tac	ccg	gaa	1680
Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	Tyr	Lys	Cys	Asp	Tyr	Pro	Glu	
		525					530					535				
agt	tat	aga	gga	acc	cta	cta	aag	gac	ttt	cac	atg	tct	gaa	tta	tcc	1728
Ser	Tyr	Arg	Gly	Thr	Leu	Leu	Lys	Asp	Phe	His	Met	Ser	Glu	Leu	Ser	
	540					545					550					
tgc	aac	ata	act	ctg	ctg	atc	gtc	acc	atc	gtt	gcc	acc	atg	ctg	gtg	1776
Cys	Asn	Ile	Thr	Leu	Leu	Ile	Val	Thr	Ile	Val	Ala	Thr	Met	Leu	Val	
555					560					565					570	
tta	gct	gtg	act	gtg	acc	tcc	ctc	tgc	atc	tac	ttg	gat	ctg	ccc	tgg	1824
Leu	Ala	Val	Thr	Val	Thr	Ser	Leu	Cys	Ile	Tyr	Leu	Asp	Leu	Pro	Trp	
				575					580					585		
tat	ctc	agg	atg	gtg	tgc	cag	tgg	acc	cag	acc	cgg	cgc	agg	gcc	agg	1872
Tyr	Leu	Arg	Met	Val	Cys	Gln	Trp	Thr	Gln	Thr	Arg	Arg	Arg	Ala	Arg	
			590					595					600			
aac	ata	ccc	tta	gaa	gaa	ctc	caa	aga	aat	ctc	cag	ttt	cat	gca	ttt	1920
Asn	Ile	Pro	Leu	Glu	Glu	Leu	Gln	Arg	Asn	Leu	Gln	Phe	His	Ala	Phe	
		605					610					615				
att	tca	tat	agt	ggg	cac	gat	tct	ttc	tgg	gtg	aag	aat	gaa	tta	ttg	1968
Ile	Ser	Tyr	Ser	Gly	His	Asp	Ser	Phe	Trp	Val	Lys	Asn	Glu	Leu	Leu	
	620					625					630					
cca	aac	cta	gag	aaa	gaa	ggg	atg	cag	att	tgc	ctt	cat	gag	aga	aac	2016
Pro	Asn	Leu	Glu	Lys	Glu	Gly	Met	Gln	Ile	Cys	Leu	His	Glu	Arg	Asn	
					640					645					650	
ttt	gtt	cct	ggc	aag	agc	att	gtg	gaa	aat	atc	atc	acc	tgc	att	gag	2064
Phe	Val	Pro	Gly	Lys	Ser	Ile	Val	Glu	Asn	Ile	Ile	Thr	Cys	Ile	Glu	
				655					660					665		
aag	agt	tac	aag	tcc	atc	ttt	gtt	ttg	tct	ccc	aac	ttt	gtc	cag	agt	2112
Lys	Ser	Tyr	Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Ser	
			670					675					680			

gaa	tgg	tgc	cat	tat	gaa	ctc	tac	ttt	gcc	cat	cac	aat	ctc	ttt	cat	2160
Glu	Trp	Cys	His	Tyr	Glu	Leu	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	
		685					690					695				

gaa	gga	tct	aat	agc	tta	atc	ctg	atc	ttg	ctg	gaa	ccc	att	ccg	cag	2208
Glu	Gly	Ser	Asn	Ser	Leu	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Gln	
	700					705					710					

tac	tcc	att	cct	agc	agt	tat	cac	aag	ctc	aaa	agt	ctc	atg	gcc	agg	2256
Tyr	Ser	Ile	Pro	Ser	Ser	Tyr	His	Lys	Leu	Lys	Ser	Leu	Met	Ala	Arg	
					720					725					730	

agg	act	tat	ttg	gaa	tgg	ccc	aag	gaa	aag	agc	aaa	cgt	ggc	ctt	ttt	2304
Arg	Thr	Tyr	Leu	Glu	Trp	Pro	Lys	Glu	Lys	Ser	Lys	Arg	Gly	Leu	Phe	
				735					740					745		

tgg	gct	aac	tta	agg	gca	gcc	att	aat	att	aag	ctg	aca	gag	caa	gca	2352
Trp	Ala	Asn	Leu	Arg	Ala	Ala	Ile	Asn	Ile	Lys	Leu	Thr	Glu	Gln	Ala	
			750					755					760			

aa	aaa	tagtctaga														2367
Lys	Lys															

<210> 2

<211> 786

<212> PRT

<213> Unknown

<400> 2

Met	Thr	Ser	Ile	Phe	His	Phe	Ala	Ile	Ile	Phe	Met	Leu	Ile	Leu	Gln	
		-20					-15					-10				

Ile	Arg	Ile	Gln	Leu	Ser	Glu	Glu	Ser	Glu	Phe	Leu	Val	Asp	Arg	Ser	
	-5				-1	1				5					10	

Lys	Asn	Gly	Leu	Ile	His	Val	Pro	Lys	Asp	Leu	Ser	Gln	Lys	Thr	Thr	
				15					20					25		

Ile	Leu	Asn	Ile	Ser	Gln	Asn	Tyr	Ile	Ser	Glu	Leu	Trp	Thr	Ser	Asp	
		30						35					40			

Ile	Leu	Ser	Leu	Ser	Lys	Leu	Arg	Ile	Leu	Ile	Ile	Ser	His	Asn	Arg	
		45					50					55				

Ile	Gln	Tyr	Leu	Asp	Ile	Ser	Val	Phe	Lys	Phe	Asn	Gln	Glu	Leu	Glu	
	60					65					70					

Tyr	Leu	Asp	Leu	Ser	His	Asn	Lys	Leu	Val	Lys	Ile	Ser	Cys	His	Pro	
	75				80					85					90	

Thr	Val	Asn	Leu	Lys	His	Leu	Asp	Leu	Ser	Phe	Asn	Ala	Phe	Asp	Ala	
				95					100					105		

Leu Pro Ile Cys Lys Glu Phe Gly Asn Met Ser Gln Leu Lys Phe Leu
 110 115 120
 Gly Leu Ser Thr Thr His Leu Glu Lys Ser Ser Val Leu Pro Ile Ala
 125 130 135
 His Leu Asn Ile Ser Lys Val Leu Leu Val Leu Gly Glu Thr Tyr Gly
 140 145 150
 Glu Lys Glu Asp Pro Glu Gly Leu Gln Asp Phe Asn Thr Glu Ser Leu
 155 160 165 170
 His Ile Val Phe Pro Thr Asn Lys Glu Phe His Phe Ile Leu Asp Val
 175 180 185
 Ser Val Lys Thr Val Ala Asn Leu Glu Leu Ser Asn Ile Lys Cys Val
 190 195 200
 Leu Glu Asp Asn Lys Cys Ser Tyr Phe Leu Ser Ile Leu Ala Lys Leu
 205 210 215
 Gln Thr Asn Pro Lys Leu Ser Ser Leu Thr Leu Asn Asn Ile Glu Thr
 220 225 230
 Thr Trp Asn Ser Phe Ile Arg Ile Leu Gln Leu Val Trp His Thr Thr
 235 240 245 250
 Val Trp Tyr Phe Ser Ile Ser Asn Val Lys Leu Gln Gly Gln Leu Asp
 255 260 265
 Phe Arg Asp Phe Asp Tyr Ser Gly Thr Ser Leu Lys Ala Leu Ser Ile
 270 275 280
 His Gln Val Val Ser Asp Val Phe Gly Phe Pro Gln Ser Tyr Ile Tyr
 285 290 295
 Glu Ile Phe Ser Asn Met Asn Ile Lys Asn Phe Thr Val Ser Gly Thr
 300 305 310
 Arg Met Val His Met Leu Cys Pro Ser Lys Ile Ser Pro Phe Leu His
 315 320 325 330
 Leu Asp Phe Ser Asn Asn Leu Leu Thr Asp Thr Val Phe Glu Asn Cys
 335 340 345
 Gly His Leu Thr Glu Leu Glu Thr Leu Ile Leu Gln Met Asn Gln Leu
 350 355 360
 Lys Glu Leu Ser Lys Ile Ala Glu Met Thr Thr Gln Met Lys Ser Leu
 365 370 375
 Gln Gln Leu Asp Ile Ser Gln Asn Ser Val Ser Tyr Asp Glu Lys Lys
 380 385 390

Gly	Asp	Cys	Ser	Trp	Thr	Lys	Ser	Leu	Leu	Ser	Leu	Asn	Met	Ser	Ser	395	400	405	410
Asn	Ile	Leu	Thr	Asp	Thr	Ile	Phe	Arg	Cys	Leu	Pro	Pro	Arg	Ile	Lys		415	420	425
Val	Leu	Asp	Leu	His	Ser	Asn	Lys	Ile	Lys	Ser	Ile	Pro	Lys	Gln	Val		430	435	440
Val	Lys	Leu	Glu	Ala	Leu	Gln	Glu	Leu	Asn	Val	Ala	Phe	Asn	Ser	Leu		445	450	455
Thr	Asp	Leu	Pro	Gly	Cys	Gly	Ser	Phe	Ser	Ser	Leu	Ser	Val	Leu	Ile		460	465	470
Ile	Asp	His	Asn	Ser	Val	Ser	His	Pro	Ser	Ala	Asp	Phe	Phe	Gln	Ser		475	480	485
Cys	Gln	Lys	Met	Arg	Ser	Ile	Lys	Ala	Gly	Asp	Asn	Pro	Phe	Gln	Cys		495	500	505
Thr	Cys	Glu	Leu	Gly	Glu	Phe	Val	Lys	Asn	Ile	Asp	Gln	Val	Ser	Ser		510	515	520
Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	Tyr	Lys	Cys	Asp	Tyr	Pro	Glu		525	530	535
Ser	Tyr	Arg	Gly	Thr	Leu	Leu	Lys	Asp	Phe	His	Met	Ser	Glu	Leu	Ser		540	545	550
Cys	Asn	Ile	Thr	Leu	Leu	Ile	Val	Thr	Ile	Val	Ala	Thr	Met	Leu	Val		555	560	565
Leu	Ala	Val	Thr	Val	Thr	Ser	Leu	Cys	Ile	Tyr	Leu	Asp	Leu	Pro	Trp		575	580	585
Tyr	Leu	Arg	Met	Val	Cys	Gln	Trp	Thr	Gln	Thr	Arg	Arg	Arg	Ala	Arg		590	595	600
Asn	Ile	Pro	Leu	Glu	Glu	Leu	Gln	Arg	Asn	Leu	Gln	Phe	His	Ala	Phe		605	610	615
Ile	Ser	Tyr	Ser	Gly	His	Asp	Ser	Phe	Trp	Val	Lys	Asn	Glu	Leu	Leu		620	625	630
Pro	Asn	Leu	Glu	Lys	Glu	Gly	Met	Gln	Ile	Cys	Leu	His	Glu	Arg	Asn		635	640	645
Phe	Val	Pro	Gly	Lys	Ser	Ile	Val	Glu	Asn	Ile	Ile	Thr	Cys	Ile	Glu		655	660	665
Lys	Ser	Tyr	Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Ser		670	675	680

Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His
 685 690 695
 Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln
 700 705 710
 Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu Met Ala Arg
 715 720 725 730
 Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe
 735 740 745
 Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr Glu Gln Ala
 750 755 760
 Lys Lys

<210> 3
 <211> 2355
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2352)

<220>
 <221> mat_peptide
 <222> (67)..(2352)

<400> 3
 atg cca cat act ttg tgg atg gtg tgg gtc ttg ggg gtc atc atc agc 48
 Met Pro His Thr Leu Trp Met Val Trp Val Leu Gly Val Ile Ile Ser
 -20 -15 -10
 ctc tcc aag gaa gaa tcc tcc aat cag gct tct ctg tct tgt gac cgc 96
 Leu Ser Lys Glu Glu Ser Ser Asn Gln Ala Ser Leu Ser Cys Asp Arg
 -5 -1 1 5 10
 aat ggt atc tgc aag ggc agc tca gga tct tta aac tcc att ccc tca 144
 Asn Gly Ile Cys Lys Gly Ser Ser Gly Ser Leu Asn Ser Ile Pro Ser
 15 20 25
 ggg ctc aca gaa gct gta aaa agc ctt gac ctg tcc aac aac agg atc 192
 Gly Leu Thr Glu Ala Val Lys Ser Leu Asp Leu Ser Asn Asn Arg Ile
 30 35 40

acc	tac	att	agc	aac	agt	gac	cta	cag	agg	tgt	gtg	aac	ctc	cag	gct	240
Thr	Tyr	Ile	Ser	Asn	Ser	Asp	Leu	Gln	Arg	Cys	Val	Asn	Leu	Gln	Ala	
		45					50					55				
ctg	gtg	ctg	aca	tcc	aat	gga	att	aac	aca	ata	gag	gaa	gat	tct	ttt	288
Leu	Val	Leu	Thr	Ser	Asn	Gly	Ile	Asn	Thr	Ile	Glu	Glu	Asp	Ser	Phe	
	60					65					70					
tct	tcc	ctg	ggc	agt	ctt	gaa	cat	tta	gac	tta	tcc	tat	aat	tac	tta	336
Ser	Ser	Leu	Gly	Ser	Leu	Glu	His	Leu	Asp	Leu	Ser	Tyr	Asn	Tyr	Leu	
75					80					85					90	
tct	aat	tta	tcg	tct	tcc	tgg	ttc	aag	ccc	ctt	tct	tct	tta	aca	ttc	384
Ser	Asn	Leu	Ser	Ser	Ser	Trp	Phe	Lys	Pro	Leu	Ser	Ser	Leu	Thr	Phe	
				95					100					105		
tta	aac	tta	ctg	gga	aat	cct	tac	aaa	acc	cta	ggg	gaa	aca	tct	ctt	432
Leu	Asn	Leu	Leu	Gly	Asn	Pro	Tyr	Lys	Thr	Leu	Gly	Glu	Thr	Ser	Leu	
			110					115					120			
ttt	tct	cat	ctc	aca	aaa	ttg	caa	atc	ctg	aga	gtg	gga	aat	atg	gac	480
Phe	Ser	His	Leu	Thr	Lys	Leu	Gln	Ile	Leu	Arg	Val	Gly	Asn	Met	Asp	
		125					130					135				
acc	ttc	act	aag	att	caa	aga	aaa	gat	ttt	gct	gga	ctt	acc	ttc	ctt	528
Thr	Phe	Thr	Lys	Ile	Gln	Arg	Lys	Asp	Phe	Ala	Gly	Leu	Thr	Phe	Leu	
	140					145					150					
gag	gaa	ctt	gag	att	gat	gct	tca	gat	cta	cag	agc	tat	gag	cca	aaa	576
Glu	Glu	Leu	Glu	Ile	Asp	Ala	Ser	Asp	Leu	Gln	Ser	Tyr	Glu	Pro	Lys	
155					160					165					170	
agt	ttg	aag	tca	att	cag	aac	gta	agt	cat	ctg	atc	ctt	cat	atg	aag	624
Ser	Leu	Lys	Ser	Ile	Gln	Asn	Val	Ser	His	Leu	Ile	Leu	His	Met	Lys	
				175					180					185		
cag	cat	att	tta	ctg	ctg	gag	att	ttt	gta	gat	gtt	aca	agt	tcc	gtg	672
Gln	His	Ile	Leu	Leu	Leu	Glu	Ile	Phe	Val	Asp	Val	Thr	Ser	Ser	Val	
			190					195					200			
gaa	tgt	ttg	gaa	ctg	cga	gat	act	gat	ttg	gac	act	ttc	cat	ttt	tca	720
Glu	Cys	Leu	Glu	Leu	Arg	Asp	Thr	Asp	Leu	Asp	Thr	Phe	His	Phe	Ser	
		205					210					215				
gaa	cta	tcc	act	ggc	gaa	aca	aat	tca	ttg	att	aaa	aag	ttt	aca	ttt	768
Glu	Leu	Ser	Thr	Gly	Glu	Thr	Asn	Ser	Leu	Ile	Lys	Lys	Phe	Thr	Phe	
	220					225					230					
aga	aat	gtg	aaa	atc	acc	gat	gaa	agt	ttg	ttt	cag	gtt	atg	aaa	ctt	816
Arg	Asn	Val	Lys	Ile	Thr	Asp	Glu	Ser	Leu	Phe	Gln	Val	Met	Lys	Leu	
235					240					245					250	
ttg	aat	cag	att	tct	gga	ttg	tta	gaa	tta	gag	ttt	gat	gac	tgt	acc	864

Leu	Asn	Gln	Ile	Ser	Gly	Leu	Leu	Glu	Leu	Glu	Phe	Asp	Asp	Cys	Thr	
				255					260					265		
ctt	aat	gga	gtt	ggt	aat	ttt	aga	gca	tct	gat	aat	gac	aga	gtt	ata	912
Leu	Asn	Gly	Val	Gly	Asn	Phe	Arg	Ala	Ser	Asp	Asn	Asp	Arg	Val	Ile	
			270					275					280			
gat	cca	ggt	aaa	gtg	gaa	acg	tta	aca	atc	cgg	agg	ctg	cat	att	cca	960
Asp	Pro	Gly	Lys	Val	Glu	Thr	Leu	Thr	Ile	Arg	Arg	Leu	His	Ile	Pro	
			285				290					295				
agg	ttt	tac	tta	ttt	tat	gat	ctg	agc	act	tta	tat	tca	ctt	aca	gaa	1008
Arg	Phe	Tyr	Leu	Phe	Tyr	Asp	Leu	Ser	Thr	Leu	Tyr	Ser	Leu	Thr	Glu	
	300					305					310					
aga	gtt	aaa	aga	atc	aca	gta	gaa	aac	agt	aaa	gtt	ttt	ctg	gtt	cct	1056
Arg	Val	Lys	Arg	Ile	Thr	Val	Glu	Asn	Ser	Lys	Val	Phe	Leu	Val	Pro	
	315				320				325						330	
tgt	tta	ctt	tca	caa	cat	tta	aaa	tca	tta	gaa	tac	ttg	gat	ctc	agt	1104
Cys	Leu	Leu	Ser	Gln	His	Leu	Lys	Ser	Leu	Glu	Tyr	Leu	Asp	Leu	Ser	
				335				340						345		
gaa	aat	ttg	atg	gtt	gaa	gaa	tac	ttg	aaa	aat	tca	gcc	tgt	gag	gat	1152
Glu	Asn	Leu	Met	Val	Glu	Glu	Tyr	Leu	Lys	Asn	Ser	Ala	Cys	Glu	Asp	
			350					355					360			
gcc	tggt	ccc	tct	cta	caa	act	tta	att	tta	agg	caa	aat	cat	ttg	gca	1200
Ala	Trp	Pro	Ser	Leu	Gln	Thr	Leu	Ile	Leu	Arg	Gln	Asn	His	Leu	Ala	
		365					370					375				
tca	ttg	gaa	aaa	acc	gga	gag	act	ttg	ctc	act	ctg	aaa	aac	ttg	act	1248
Ser	Leu	Glu	Lys	Thr	Gly	Glu	Thr	Leu	Leu	Thr	Leu	Lys	Asn	Leu	Thr	
	380				385						390					
aac	att	gat	atc	agt	aag	aat	agt	ttt	cat	tct	atg	cct	gaa	act	tgt	1296
Asn	Ile	Asp	Ile	Ser	Lys	Asn	Ser	Phe	His	Ser	Met	Pro	Glu	Thr	Cys	
					400					405					410	
cag	tggt	cca	gaa	aag	atg	aaa	tat	ttg	aac	tta	tcc	agc	aca	cga	ata	1344
Gln	Trp	Pro	Glu	Lys	Met	Lys	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Arg	Ile	
				415				420						425		
cac	agt	gta	aca	ggc	tgc	att	ccc	aag	aca	ctg	gaa	att	tta	gat	gtt	1392
His	Ser	Val	Thr	Gly	Cys	Ile	Pro	Lys	Thr	Leu	Glu	Ile	Leu	Asp	Val	
			430					435					440			
agc	aac	aac	aat	ctc	aat	tta	ttt	tct	ttg	aat	ttg	cgg	caa	ctc	aaa	1440
Ser	Asn	Asn	Asn	Leu	Asn	Leu	Phe	Ser	Leu	Asn	Leu	Pro	Gln	Leu	Lys	
			445				450					455				
gaa	ctt	tat	att	tcc	aga	aat	aag	ttg	atg	act	cta	cca	gat	gcc	tcc	1488
Glu	Leu	Tyr	Ile	Ser	Arg	Asn	Lys	Leu	Met	Thr	Leu	Pro	Asp	Ala	Ser	

460				465				470								
ctc	tta	ccc	atg	tta	cta	gta	ttg	aaa	atc	agt	agg	aat	gca	ata	act	1536
Leu	Leu	Pro	Met	Leu	Leu	Val	Leu	Lys	Ile	Ser	Arg	Asn	Ala	Ile	Thr	
475				480						485					490	
acg	ttt	tct	aag	gag	caa	ctt	gac	tca	ttt	cac	aca	ctg	aag	act	ttg	1584
Thr	Phe	Ser	Lys	Glu	Gln	Leu	Asp	Ser	Phe	His	Thr	Leu	Lys	Thr	Leu	
				495					500					505		
gaa	gct	ggt	ggc	aat	aac	ttc	att	tgc	tcc	tgt	gaa	ttc	ctc	tcc	ttc	1632
Glu	Ala	Gly	Gly	Asn	Asn	Phe	Ile	Cys	Ser	Cys	Glu	Phe	Leu	Ser	Phe	
			510					515					520			
act	cag	gag	cag	caa	gca	ctg	gcc	aaa	gtc	ttg	att	gat	tgg	cca	gca	1680
Thr	Gln	Glu	Gln	Gln	Ala	Leu	Ala	Lys	Val	Leu	Ile	Asp	Trp	Pro	Ala	
		525					530					535				
aat	tac	ctg	tgt	gac	tct	cca	tcc	cat	gtg	cgt	ggc	cag	cag	gtt	cag	1728
Asn	Tyr	Leu	Cys	Asp	Ser	Pro	Ser	His	Val	Arg	Gly	Gln	Gln	Val	Gln	
	540					545					550					
gat	gtc	cgc	ctc	tcg	gtg	tcg	gaa	tgt	cac	agg	aca	gca	ctg	gtg	tct	1776
Asp	Val	Arg	Leu	Ser	Val	Ser	Glu	Cys	His	Arg	Thr	Ala	Leu	Val	Ser	
555					560					565					570	
ggc	atg	tgc	tgt	gct	ctg	ttc	ctg	ctg	atc	ctg	ctc	acg	ggg	gtc	ctg	1824
Gly	Met	Cys	Cys	Ala	Leu	Phe	Leu	Leu	Ile	Leu	Leu	Thr	Gly	Val	Leu	
				575					580					585		
tgc	cac	cgt	ttc	cat	ggc	ctg	tgg	tat	atg	aaa	atg	atg	tgg	gcc	tgg	1872
Cys	His	Arg	Phe	His	Gly	Leu	Trp	Tyr	Met	Lys	Met	Met	Trp	Ala	Trp	
			590					595					600			
ctc	cag	gcc	aaa	agg	aag	ccc	agg	aaa	gct	ccc	agc	agg	aac	atc	tgc	1920
Leu	Gln	Ala	Lys	Arg	Lys	Pro	Arg	Lys	Ala	Pro	Ser	Arg	Asn	Ile	Cys	
		605					610					615				
tat	gat	gca	ttt	gtt	tct	tac	agt	gag	cgg	gat	gcc	tac	tgg	gtg	gag	1968
Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Glu	Arg	Asp	Ala	Tyr	Trp	Val	Glu	
	620					625					630					
aac	ctt	atg	gtc	cag	gag	ctg	gag	aac	ttc	aat	ccc	ccc	ttc	aag	ttg	2016
Asn	Leu	Met	Val	Gln	Glu	Leu	Glu	Asn	Phe	Asn	Pro	Pro	Phe	Lys	Leu	
635					640					645				650		
tgt	ctt	cat	aag	cgg	gac	ttc	att	cct	ggc	aag	tgg	atc	att	gac	aat	2064
Cys	Leu	His	Lys	Arg	Asp	Phe	Ile	Pro	Gly	Lys	Trp	Ile	Ile	Asp	Asn	
				655					660					665		
atc	att	gac	tcc	att	gaa	aag	agc	cac	aaa	act	gtc	ttt	gtg	ctt	tct	2112
Ile	Ile	Asp	Ser	Ile	Glu	Lys	Ser	His	Lys	Thr	Val	Phe	Val	Leu	Ser	
			670					675					680			

gaa aac ttt gtg aag agt gag tgg tgc aag tat gaa ctg gac ttc tcc	2160
Glu Asn Phe Val Lys Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser	
685 690 695	

cat ttc cgt ctt ttt gaa gag aac aat gat gct gcc att ctc att ctt	2208
His Phe Arg Leu Phe Glu Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu	
700 705 710	

ctg gag ccc att gag aaa aaa gcc att ccc cag cgc ttc tgc aag ctg	2256
Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu	
715 720 725 730	

cgg aag ata atg aac acc aag acc tac ctg gag tgg ccc atg gac gag	2304
Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu	
735 740 745	

gct cag cgg gaa gga ttt tgg gta aat ctg aga gct gcg ata aag tcc	2352
Ala Gln Arg Glu Gly Phe Trp Val Asn Leu Arg Ala Ala Ile Lys Ser	
750 755 760	

tag	2355
-----	------

<210> 4
 <211> 784
 <212> PRT
 <213> Unknown

<400> 4	
Met Pro His Thr Leu Trp Met Val Trp Val Leu Gly Val Ile Ile Ser	
-20 -15 -10	

Leu Ser Lys Glu Glu Ser Ser Asn Gln Ala Ser Leu Ser Cys Asp Arg	
-5 -1 1 5 10	

Asn Gly Ile Cys Lys Gly Ser Ser Gly Ser Leu Asn Ser Ile Pro Ser	
15 20 25	

Gly Leu Thr Glu Ala Val Lys Ser Leu Asp Leu Ser Asn Asn Arg Ile	
30 35 40	

Thr Tyr Ile Ser Asn Ser Asp Leu Gln Arg Cys Val Asn Leu Gln Ala	
45 50 55	

Leu Val Leu Thr Ser Asn Gly Ile Asn Thr Ile Glu Glu Asp Ser Phe	
60 65 70	

Ser Ser Leu Gly Ser Leu Glu His Leu Asp Leu Ser Tyr Asn Tyr Leu	
75 80 85 90	

Ser Asn Leu Ser Ser Ser Trp Phe Lys Pro Leu Ser Ser Leu Thr Phe	
95 100 105	

Leu Asn Leu Leu Gly Asn Pro Tyr Lys Thr Leu Gly Glu Thr Ser Leu
 110 115 120
 Phe Ser His Leu Thr Lys Leu Gln Ile Leu Arg Val Gly Asn Met Asp
 125 130 135
 Thr Phe Thr Lys Ile Gln Arg Lys Asp Phe Ala Gly Leu Thr Phe Leu
 140 145 150
 Glu Glu Leu Glu Ile Asp Ala Ser Asp Leu Gln Ser Tyr Glu Pro Lys
 155 160 165 170
 Ser Leu Lys Ser Ile Gln Asn Val Ser His Leu Ile Leu His Met Lys
 175 180 185
 Gln His Ile Leu Leu Leu Glu Ile Phe Val Asp Val Thr Ser Ser Val
 190 195 200
 Glu Cys Leu Glu Leu Arg Asp Thr Asp Leu Asp Thr Phe His Phe Ser
 205 210 215
 Glu Leu Ser Thr Gly Glu Thr Asn Ser Leu Ile Lys Lys Phe Thr Phe
 220 225 230
 Arg Asn Val Lys Ile Thr Asp Glu Ser Leu Phe Gln Val Met Lys Leu
 235 240 245 250
 Leu Asn Gln Ile Ser Gly Leu Leu Glu Leu Glu Phe Asp Asp Cys Thr
 255 260 265
 Leu Asn Gly Val Gly Asn Phe Arg Ala Ser Asp Asn Asp Arg Val Ile
 270 275 280
 Asp Pro Gly Lys Val Glu Thr Leu Thr Ile Arg Arg Leu His Ile Pro
 285 290 295
 Arg Phe Tyr Leu Phe Tyr Asp Leu Ser Thr Leu Tyr Ser Leu Thr Glu
 300 305 310
 Arg Val Lys Arg Ile Thr Val Glu Asn Ser Lys Val Phe Leu Val Pro
 315 320 325 330
 Cys Leu Leu Ser Gln His Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
 335 340 345
 Glu Asn Leu Met Val Glu Glu Tyr Leu Lys Asn Ser Ala Cys Glu Asp
 350 355 360
 Ala Trp Pro Ser Leu Gln Thr Leu Ile Leu Arg Gln Asn His Leu Ala
 365 370 375
 Ser Leu Glu Lys Thr Gly Glu Thr Leu Leu Thr Leu Lys Asn Leu Thr
 380 385 390

Asn	Ile	Asp	Ile	Ser	Lys	Asn	Ser	Phe	His	Ser	Met	Pro	Glu	Thr	Cys	
395					400					405					410	
Gln	Trp	Pro	Glu	Lys	Met	Lys	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Arg	Ile	
				415					420					425		
His	Ser	Val	Thr	Gly	Cys	Ile	Pro	Lys	Thr	Leu	Glu	Ile	Leu	Asp	Val	
			430					435					440			
Ser	Asn	Asn	Asn	Leu	Asn	Leu	Phe	Ser	Leu	Asn	Leu	Pro	Gln	Leu	Lys	
		445					450					455				
Glu	Leu	Tyr	Ile	Ser	Arg	Asn	Lys	Leu	Met	Thr	Leu	Pro	Asp	Ala	Ser	
	460					465					470					
Leu	Leu	Pro	Met	Leu	Leu	Val	Leu	Lys	Ile	Ser	Arg	Asn	Ala	Ile	Thr	
475					480					485					490	
Thr	Phe	Ser	Lys	Glu	Gln	Leu	Asp	Ser	Phe	His	Thr	Leu	Lys	Thr	Leu	
				495					500					505		
Glu	Ala	Gly	Gly	Asn	Asn	Phe	Ile	Cys	Ser	Cys	Glu	Phe	Leu	Ser	Phe	
			510					515					520			
Thr	Gln	Glu	Gln	Gln	Ala	Leu	Ala	Lys	Val	Leu	Ile	Asp	Trp	Pro	Ala	
		525					530					535				
Asn	Tyr	Leu	Cys	Asp	Ser	Pro	Ser	His	Val	Arg	Gly	Gln	Gln	Val	Gln	
	540					545					550					
Asp	Val	Arg	Leu	Ser	Val	Ser	Glu	Cys	His	Arg	Thr	Ala	Leu	Val	Ser	
555					560					565					570	
Gly	Met	Cys	Cys	Ala	Leu	Phe	Leu	Leu	Ile	Leu	Leu	Thr	Gly	Val	Leu	
				575					580					585		
Cys	His	Arg	Phe	His	Gly	Leu	Trp	Tyr	Met	Lys	Met	Met	Trp	Ala	Trp	
			590					595					600			
Leu	Gln	Ala	Lys	Arg	Lys	Pro	Arg	Lys	Ala	Pro	Ser	Arg	Asn	Ile	Cys	
		605					610					615				
Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Glu	Arg	Asp	Ala	Tyr	Trp	Val	Glu	
	620					625					630					
Asn	Leu	Met	Val	Gln	Glu	Leu	Glu	Asn	Phe	Asn	Pro	Pro	Phe	Lys	Leu	
635					640					645					650	
Cys	Leu	His	Lys	Arg	Asp	Phe	Ile	Pro	Gly	Lys	Trp	Ile	Ile	Asp	Asn	
				655					660					665		
Ile	Ile	Asp	Ser	Ile	Glu	Lys	Ser	His	Lys	Thr	Val	Phe	Val	Leu	Ser	
			670					675					680			

Glu	Asn	Phe	Val	Lys	Ser	Glu	Trp	Cys	Lys	Tyr	Glu	Leu	Asp	Phe	Ser
		685					690					695			
His	Phe	Arg	Leu	Phe	Glu	Glu	Asn	Asn	Asp	Ala	Ala	Ile	Leu	Ile	Leu
	700					705					710				
Leu	Glu	Pro	Ile	Glu	Lys	Lys	Ala	Ile	Pro	Gln	Arg	Phe	Cys	Lys	Leu
	715				720					725					730
Arg	Lys	Ile	Met	Asn	Thr	Lys	Thr	Tyr	Leu	Glu	Trp	Pro	Met	Asp	Glu
				735					740					745	
Ala	Gln	Arg	Glu	Gly	Phe	Trp	Val	Asn	Leu	Arg	Ala	Ala	Ile	Lys	Ser
			750					755						760	

<210> 5

<211> 2715

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (1)..(2712)

<220>

<221> mat_peptide

<222> (64)..(2712)

<400> 5

atg	aga	cag	act	ttg	cct	tgt	atc	tac	ttt	tgg	ggg	ggc	ctt	ttg	ccc	48
Met	Arg	Gln	Thr	Leu	Pro	Cys	Ile	Tyr	Phe	Trp	Gly	Gly	Leu	Leu	Pro	
	-20					-15					-10					

ttt	ggg	atg	ctg	tgt	gca	tcc	tcc	acc	acc	aag	tgc	act	gtt	agc	cat	96
Phe	Gly	Met	Leu	Cys	Ala	Ser	Ser	Thr	Thr	Lys	Cys	Thr	Val	Ser	His	
-5			-1	1				5					10			

gaa	gtt	gct	gac	tgc	agc	cac	ctg	aag	ttg	act	cag	gta	ccc	gat	gat	144
Glu	Val	Ala	Asp	Cys	Ser	His	Leu	Lys	Leu	Thr	Gln	Val	Pro	Asp	Asp	
		15					20					25				

cta	ccc	aca	aac	ata	aca	gtg	ttg	aac	ctt	acc	cat	aat	caa	ctc	aga	192
Leu	Pro	Thr	Asn	Ile	Thr	Val	Leu	Asn	Leu	Thr	His	Asn	Gln	Leu	Arg	
		30				35					40					

aga	tta	cca	gcc	gcc	aac	ttc	aca	agg	tat	agc	cag	cta	act	agc	ttg	240
Arg	Leu	Pro	Ala	Ala	Asn	Phe	Thr	Arg	Tyr	Ser	Gln	Leu	Thr	Ser	Leu	
45						50					55					

gat	gta	gga	ttt	aac	acc	atc	tca	aaa	ctg	gag	cca	gaa	ttg	tgc	cag	288
Asp	Val	Gly	Phe	Asn	Thr	Ile	Ser	Lys	Leu	Glu	Pro	Glu	Leu	Cys	Gln	
60					65					70					75	
aaa	ctt	ccc	atg	tta	aaa	ggt	ttg	aac	ctc	cag	cac	aat	gag	cta	tct	336
Lys	Leu	Pro	Met	Leu	Lys	Val	Leu	Asn	Leu	Gln	His	Asn	Glu	Leu	Ser	
				80					85					90		
caa	ctt	tct	gat	aaa	acc	ttt	gcc	ttc	tgc	acg	aat	ttg	act	gaa	ctc	384
Gln	Leu	Ser	Asp	Lys	Thr	Phe	Ala	Phe	Cys	Thr	Asn	Leu	Thr	Glu	Leu	
			95					100					105			
cat	ctc	atg	tcc	aac	tca	atc	cag	aaa	att	aaa	aat	aat	ccc	ttt	gtc	432
His	Leu	Met	Ser	Asn	Ser	Ile	Gln	Lys	Ile	Lys	Asn	Asn	Pro	Phe	Val	
		110					115					120				
aag	cag	aag	aat	tta	atc	aca	tta	gat	ctg	tct	cat	aat	ggc	ttg	tca	480
Lys	Gln	Lys	Asn	Leu	Ile	Thr	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	Ser	
	125					130					135					
tct	aca	aaa	tta	gga	act	cag	ggt	cag	ctg	gaa	aat	ctc	caa	gag	ctt	528
Ser	Thr	Lys	Leu	Gly	Thr	Gln	Val	Gln	Leu	Glu	Asn	Leu	Gln	Glu	Leu	
140					145					150					155	
cta	tta	tca	aac	aat	aaa	att	caa	gcg	cta	aaa	agt	gaa	gaa	ctg	gat	576
Leu	Leu	Ser	Asn	Asn	Lys	Ile	Gln	Ala	Leu	Lys	Ser	Glu	Glu	Leu	Asp	
				160					165					170		
atc	ttt	gcc	aat	tca	tct	tta	aaa	aaa	tta	gag	ttg	tca	tcg	aat	caa	624
Ile	Phe	Ala	Asn	Ser	Ser	Leu	Lys	Lys	Leu	Glu	Leu	Ser	Ser	Asn	Gln	
			175					180					185			
att	aaa	gag	ttt	tct	cca	ggg	tgt	ttt	cac	gca	att	gga	aga	tta	ttt	672
Ile	Lys	Glu	Phe	Ser	Pro	Gly	Cys	Phe	His	Ala	Ile	Gly	Arg	Leu	Phe	
		190					195					200				
ggc	ctc	ttt	ctg	aac	aat	gtc	cag	ctg	ggt	ccc	agc	ctt	aca	gag	aag	720
Gly	Leu	Phe	Leu	Asn	Asn	Val	Gln	Leu	Gly	Pro	Ser	Leu	Thr	Glu	Lys	
	205					210					215					
cta	tgt	ttg	gaa	tta	gca	aac	aca	agc	att	cgg	aat	ctg	tct	ctg	agt	768
Leu	Cys	Leu	Glu	Leu	Ala	Asn	Thr	Ser	Ile	Arg	Asn	Leu	Ser	Leu	Ser	
220					225				230						235	
aac	agc	cag	ctg	tcc	acc	acc	agc	aat	aca	act	ttc	ttg	gga	cta	aag	816
Asn	Ser	Gln	Leu	Ser	Thr	Thr	Ser	Asn	Thr	Thr	Phe	Leu	Gly	Leu	Lys	
				240					245					250		
tgg	aca	aat	ctc	act	atg	ctc	gat	ctt	tcc	tac	aac	aac	tta	aat	gtg	864
Trp	Thr	Asn	Leu	Thr	Met	Leu	Asp	Leu	Ser	Tyr	Asn	Asn	Leu	Asn	Val	
			255					260					265			

gtt	ggt	aac	gat	tcc	ttt	gct	tgg	ctt	cca	caa	cta	gaa	tat	ttc	ttc	912
Val	Gly	Asn	Asp	Ser	Phe	Ala	Trp	Leu	Pro	Gln	Leu	Glu	Tyr	Phe	Phe	
		270					275					280				
cta	gag	tat	aat	aat	ata	cag	cat	ttg	ttt	tct	cac	tct	ttg	cac	ggg	960
Leu	Glu	Tyr	Asn	Asn	Ile	Gln	His	Leu	Phe	Ser	His	Ser	Leu	His	Gly	
	285					290					295					
ctt	ttc	aat	gtg	agg	tac	ctg	aat	ttg	aaa	cgg	tct	ttt	act	aaa	caa	1008
Leu	Phe	Asn	Val	Arg	Tyr	Leu	Asn	Leu	Lys	Arg	Ser	Phe	Thr	Lys	Gln	
300					305					310					315	
agt	att	tcc	ctt	gcc	tca	ctc	ccc	aag	att	gat	gat	ttt	tct	ttt	cag	1056
Ser	Ile	Ser	Leu	Ala	Ser	Leu	Pro	Lys	Ile	Asp	Asp	Phe	Ser	Phe	Gln	
				320					325					330		
tgg	cta	aaa	tgt	ttg	gag	cac	ctt	aac	atg	gaa	gat	aat	gat	att	cca	1104
Trp	Leu	Lys	Cys	Leu	Glu	His	Leu	Asn	Met	Glu	Asp	Asn	Asp	Ile	Pro	
		335						340					345			
ggc	ata	aaa	agc	aat	atg	ttc	aca	gga	ttg	ata	aac	ctg	aaa	tac	tta	1152
Gly	Ile	Lys	Ser	Asn	Met	Phe	Thr	Gly	Leu	Ile	Asn	Leu	Lys	Tyr	Leu	
		350					355					360				
agt	cta	tcc	aac	tcc	ttt	aca	agt	ttg	cga	act	ttg	aca	aat	gaa	aca	1200
Ser	Leu	Ser	Asn	Ser	Phe	Thr	Ser	Leu	Arg	Thr	Leu	Thr	Asn	Glu	Thr	
	365					370					375					
ttt	gta	tca	ctt	gct	cat	tct	ccc	tta	cac	ata	ctc	aac	cta	acc	aag	1248
Phe	Val	Ser	Leu	Ala	His	Ser	Pro	Leu	His	Ile	Leu	Asn	Leu	Thr	Lys	
380					385					390					395	
aat	aaa	atc	tca	aaa	ata	gag	agt	gat	gct	ttc	tct	tgg	ttg	ggc	cac	1296
Asn	Lys	Ile	Ser	Lys	Ile	Glu	Ser	Asp	Ala	Phe	Ser	Trp	Leu	Gly	His	
				400					405					410		
cta	gaa	gta	ctt	gac	ctg	ggc	ctt	aat	gaa	att	ggg	caa	gaa	ctc	aca	1344
Leu	Glu	Val	Leu	Asp	Leu	Gly	Leu	Asn	Glu	Ile	Gly	Gln	Glu	Leu	Thr	
		415						420					425			
ggc	cag	gaa	tgg	aga	ggt	cta	gaa	aat	att	ttc	gaa	atc	tat	ctt	tcc	1392
Gly	Gln	Glu	Trp	Arg	Gly	Leu	Glu	Asn	Ile	Phe	Glu	Ile	Tyr	Leu	Ser	
		430					435					440				
tac	aac	aag	tac	ctg	cag	ctg	act	agg	aac	tcc	ttt	gcc	ttg	gtc	cca	1440
Tyr	Asn	Lys	Tyr	Leu	Gln	Leu	Thr	Arg	Asn	Ser	Phe	Ala	Leu	Val	Pro	
	445					450					455					
agc	ctt	caa	cga	ctg	atg	ctc	cga	agg	gtg	gcc	ctt	aaa	aat	gtg	gat	1488
Ser	Leu	Gln	Arg	Leu	Met	Leu	Arg	Arg	Val	Ala	Leu	Lys	Asn	Val	Asp	
460					465				470						475	
agc	tct	cct	tca	cca	ttc	cag	cct	ctt	cgt	aac	ttg	acc	att	ctg	gat	1536
Ser	Ser	Pro	Ser	Pro	Phe	Gln	Pro	Leu	Arg	Asn	Leu	Thr	Ile	Leu	Asp	

480								485				490						
cta	agc	aac	aac	aac	ata	gcc	aac	ata	aat	gat	gac	atg	ttg	gag	ggt	1584		
Leu	Ser	Asn	Asn	Asn	Ile	Ala	Asn	Ile	Asn	Asp	Asp	Met	Leu	Glu	Gly			
			495					500					505					
ctt	gag	aaa	cta	gaa	att	ctc	gat	ttg	cag	cat	aac	aac	tta	gca	cgg	1632		
Leu	Glu	Lys	Leu	Glu	Ile	Leu	Asp	Leu	Gln	His	Asn	Asn	Leu	Ala	Arg			
		510					515					520						
ctc	tgg	aaa	cac	gca	aac	cct	ggt	ggt	ccc	att	tat	ttc	cta	aag	ggt	1680		
Leu	Trp	Lys	His	Ala	Asn	Pro	Gly	Gly	Pro	Ile	Tyr	Phe	Leu	Lys	Gly			
	525					530					535							
ctg	tct	cac	ctc	cac	atc	ctt	aac	ttg	gag	tcc	aac	ggc	ttt	gac	gag	1728		
Leu	Ser	His	Leu	His	Ile	Leu	Asn	Leu	Glu	Ser	Asn	Gly	Phe	Asp	Glu			
540					545					550					555			
atc	cca	gtt	gag	gtc	ttc	aag	gat	tta	ttt	gaa	cta	aag	atc	atc	gat	1776		
Ile	Pro	Val	Glu	Val	Phe	Lys	Asp	Leu	Phe	Glu	Leu	Lys	Ile	Ile	Asp			
				560					565					570				
tta	gga	ttg	aat	aat	tta	aac	aca	ctt	cca	gca	tct	gtc	ttt	aat	aat	1824		
Leu	Gly	Leu	Asn	Asn	Leu	Asn	Thr	Leu	Pro	Ala	Ser	Val	Phe	Asn	Asn			
			575					580					585					
cag	gtg	tct	cta	aag	tca	ttg	aac	ctt	cag	aag	aat	ctc	ata	aca	tcc	1872		
Gln	Val	Ser	Leu	Lys	Ser	Leu	Asn	Leu	Gln	Lys	Asn	Leu	Ile	Thr	Ser			
		590					595					600						
gat	gag	aag	aag	gtt	ttc	ggg	cca	gct	ttc	agg	aac	ctg	act	gag	tta	1920		
Val	Glu	Lys	Lys	Val	Phe	Gly	Pro	Ala	Phe	Arg	Asn	Leu	Thr	Glu	Leu			
	605					610					615							
gat	atg	cgc	ttt	aat	ccc	ttt	gat	tgc	acg	tgt	gaa	agt	att	gcc	tgg	1968		
Asp	Met	Arg	Phe	Asn	Pro	Phe	Asp	Cys	Thr	Cys	Glu	Ser	Ile	Ala	Trp			
620					625					630					635			
ttt	gtt	aat	tgg	att	aac	gag	acc	cat	acc	aac	atc	cct	gag	ctg	tca	2016		
Phe	Val	Asn	Trp	Ile	Asn	Glu	Thr	His	Thr	Asn	Ile	Pro	Glu	Leu	Ser			
				640					645					650				
agc	cac	tac	ctt	tgc	aac	act	cca	cct	cac	tat	cat	ggg	ttc	cca	gtg	2064		
Ser	His	Tyr	Leu	Cys	Asn	Thr	Pro	Pro	His	Tyr	His	Gly	Phe	Pro	Val			
			655					660					665					
aga	ctt	ttt	gat	aca	tca	tct	tgc	aaa	gac	agt	gcc	ccc	ttt	gaa	ctc	2112		
Arg	Leu	Phe	Asp	Thr	Ser	Ser	Cys	Lys	Asp	Ser	Ala	Pro	Phe	Glu	Leu			
		670					675					680						
ttt	ttc	atg	atc	aat	acc	agt	atc	ctg	ttg	att	ttt	atc	ttt	att	gta	2160		
Phe	Phe	Met	Ile	Asn	Thr	Ser	Ile	Leu	Leu	Ile	Phe	Ile	Phe	Ile	Val			
	685					690					695							

ctt ctc atc cac ttt gag ggc tgg agg ata tct ttt tat tgg aat gtt	2208
Leu Leu Ile His Phe Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn Val	
700 705 710 715	
tca gta cat cga gtt ctt ggt ttc aaa gaa ata gac aga cag aca gaa	2256
Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu	
720 725 730	
cag ttt gaa tat gca gca tat ata att cat gcc tat aaa gat aag gat	2304
Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp	
735 740 745	
tgg gtc tgg gaa cat ttc tct tca atg gaa aag gaa gac caa tct ctc	2352
Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu	
750 755 760	
aaa ttt tgt ctg gaa gaa agg gac ttt gag gcg ggt gtt ttt gaa cta	2400
Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu	
765 770 775	
gaa gca att gtt aac agc atc aaa aga agc aga aaa att att ttt gtt	2448
Gln Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val	
780 785 790 795	
ata aca cac cat cta tta aaa gac cca tta tgc aaa aga ttc aag gta	2496
Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val	
800 805 810	
cat cat gca gtt caa caa gct att gaa caa aat ctg gat tcc att ata	2544
His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile	
815 820 825	
tgg gtt ttc ctt gag gag att cca gat tat aaa ctg aac cat gca ctc	2592
Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu	
830 835 840	
tgt ttg cga aga gga atg ttt aaa tct cac tgc atc ttg aac tgg cca	2640
Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro	
845 850 855	
gtt cag aaa gaa cgg ata ggt gcc ttt cgt cat aaa ttg caa gta gca	2688
Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala	
860 865 870 875	
ctt gga tcc aaa aac tct gta cat taa	2715
Leu Gly Ser Lys Asn Ser Val His	
880	

<210> 6

<211> 904

<212> PRT

<213> Unknown

<400> 6

Met	Arg	Gln	Thr	Leu	Pro	Cys	Ile	Tyr	Phe	Trp	Gly	Gly	Leu	Leu	Pro	
-20						-15					-10					
Phe	Gly	Met	Leu	Cys	Ala	Ser	Ser	Thr	Thr	Lys	Cys	Thr	Val	Ser	His	
-5				-1	1				5					10		
Glu	Val	Ala	Asp	Cys	Ser	His	Leu	Lys	Leu	Thr	Gln	Val	Pro	Asp	Asp	
			15					20					25			
Leu	Pro	Thr	Asn	Ile	Thr	Val	Leu	Asn	Leu	Thr	His	Asn	Gln	Leu	Arg	
		30					35					40				
Arg	Leu	Pro	Ala	Ala	Asn	Phe	Thr	Arg	Tyr	Ser	Gln	Leu	Thr	Ser	Leu	
	45					50					55					
Asp	Val	Gly	Phe	Asn	Thr	Ile	Ser	Lys	Leu	Glu	Pro	Glu	Leu	Cys	Gln	
60					65					70					75	
Lys	Leu	Pro	Met	Leu	Lys	Val	Leu	Asn	Leu	Gln	His	Asn	Glu	Leu	Ser	
				80					85					90		
Gln	Leu	Ser	Asp	Lys	Thr	Phe	Ala	Phe	Cys	Thr	Asn	Leu	Thr	Glu	Leu	
			95					100					105			
His	Leu	Met	Ser	Asn	Ser	Ile	Gln	Lys	Ile	Lys	Asn	Asn	Pro	Phe	Val	
		110					115					120				
Lys	Gln	Lys	Asn	Leu	Ile	Thr	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	Ser	
	125					130					135					
Ser	Thr	Lys	Leu	Gly	Thr	Gln	Val	Gln	Leu	Glu	Asn	Leu	Gln	Glu	Leu	
140					145					150					155	
Leu	Leu	Ser	Asn	Asn	Lys	Ile	Gln	Ala	Leu	Lys	Ser	Glu	Glu	Leu	Asp	
				160					165					170		
Ile	Phe	Ala	Asn	Ser	Ser	Leu	Lys	Lys	Leu	Glu	Leu	Ser	Ser	Asn	Gln	
			175					180					185			
Ile	Lys	Glu	Phe	Ser	Pro	Gly	Cys	Phe	His	Ala	Ile	Gly	Arg	Leu	Phe	
	190						195					200				
Gly	Leu	Phe	Leu	Asn	Asn	Val	Gln	Leu	Gly	Pro	Ser	Leu	Thr	Glu	Lys	
	205					210					215					
Leu	Cys	Leu	Glu	Leu	Ala	Asn	Thr	Ser	Ile	Arg	Asn	Leu	Ser	Leu	Ser	
220					225					230					235	
Asn	Ser	Gln	Leu	Ser	Thr	Thr	Ser	Asn	Thr	Thr	Phe	Leu	Gly	Leu	Lys	
				240					245					250		

Trp	Thr	Asn	Leu	Thr	Met	Leu	Asp	Leu	Ser	Tyr	Asn	Asn	Leu	Asn	Val
			255					260					265		
Val	Gly	Asn	Asp	Ser	Phe	Ala	Trp	Leu	Pro	Gln	Leu	Glu	Tyr	Phe	Phe
		270					275					280			
Leu	Glu	Tyr	Asn	Asn	Ile	Gln	His	Leu	Phe	Ser	His	Ser	Leu	His	Gly
	285					290					295				
Leu	Phe	Asn	Val	Arg	Tyr	Leu	Asn	Leu	Lys	Arg	Ser	Phe	Thr	Lys	Gln
300					305					310					315
Ser	Ile	Ser	Leu	Ala	Ser	Leu	Pro	Lys	Ile	Asp	Asp	Phe	Ser	Phe	Gln
				320					325					330	
Trp	Leu	Lys	Cys	Leu	Glu	His	Leu	Asn	Met	Glu	Asp	Asn	Asp	Ile	Pro
			335					340					345		
Gly	Ile	Lys	Ser	Asn	Met	Phe	Thr	Gly	Leu	Ile	Asn	Leu	Lys	Tyr	Leu
		350					355					360			
Ser	Leu	Ser	Asn	Ser	Phe	Thr	Ser	Leu	Arg	Thr	Leu	Thr	Asn	Glu	Thr
365						370					375				
Phe	Val	Ser	Leu	Ala	His	Ser	Pro	Leu	His	Ile	Leu	Asn	Leu	Thr	Lys
380					385					390					395
Asn	Lys	Ile	Ser	Lys	Ile	Glu	Ser	Asp	Ala	Phe	Ser	Trp	Leu	Gly	His
				400					405					410	
Leu	Glu	Val	Leu	Asp	Leu	Gly	Leu	Asn	Glu	Ile	Gly	Gln	Glu	Leu	Thr
			415					420					425		
Gly	Gln	Glu	Trp	Arg	Gly	Leu	Glu	Asn	Ile	Phe	Glu	Ile	Tyr	Leu	Ser
		430					435					440			
Tyr	Asn	Lys	Tyr	Leu	Gln	Leu	Thr	Arg	Asn	Ser	Phe	Ala	Leu	Val	Pro
	445					450					455				
Ser	Leu	Gln	Arg	Leu	Met	Leu	Arg	Arg	Val	Ala	Leu	Lys	Asn	Val	Asp
460					465					470					475
Ser	Ser	Pro	Ser	Pro	Phe	Gln	Pro	Leu	Arg	Asn	Leu	Thr	Ile	Leu	Asp
				480					485					490	
Leu	Ser	Asn	Asn	Asn	Ile	Ala	Asn	Ile	Asn	Asp	Asp	Met	Leu	Glu	Gly
			495					500					505		
Leu	Glu	Lys	Leu	Glu	Ile	Leu	Asp	Leu	Gln	His	Asn	Asn	Leu	Ala	Arg
		510					515					520			
Leu	Trp	Lys	His	Ala	Asn	Pro	Gly	Gly	Pro	Ile	Tyr	Phe	Leu	Lys	Gly
	525					530					535				

Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Phe Asp Glu
 540 545 550 555
 Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp
 560 565 570
 Leu Gly Leu Asn Asn Leu Asn Thr Leu Pro Ala Ser Val Phe Asn Asn
 575 580 585
 Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser
 590 595 600
 Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu
 605 610 615
 Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp
 620 625 630 635
 Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser
 640 645 650
 Ser His Tyr Leu Cys Asn Thr Pro Pro His Tyr His Gly Phe Pro Val
 655 660 665
 Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu Leu
 670 675 680
 Phe Phe Met Ile Asn Thr Ser Ile Leu Leu Ile Phe Ile Phe Ile Val
 685 690 695
 Leu Leu Ile His Phe Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn Val
 700 705 710 715
 Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu
 720 725 730
 Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp
 735 740 745
 Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu
 750 755 760
 Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu
 765 770 775
 Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val
 780 785 790 795
 Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val
 800 805 810
 His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile
 815 820 825

Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu
 830 835 840
 Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro
 845 850 855
 Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala
 860 865 870 875
 Leu Gly Ser Lys Asn Ser Val His
 880

<210> 7
 <211> 2400
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (2397)

<400> 7
 atg gag ctg aat ttc tac aaa atc ccc gac aac ctc ccc ttc tca acc 48
 Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro Phe Ser Thr
 5 10 15
 aag aac ctg gac ctg agc ttt aat ccc ctg agg cat tta ggc agc tat 96
 Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr
 20 25 30
 agc ttc ttc agt ttc cca gaa ctg cag gtg ctg gat tta tcc agg tgt 144
 Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys
 35 40 45
 gaa atc cag aca att gaa gat ggg gca tat cag agc cta agc cac ctc 192
 Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu
 50 55 60
 tct acc tta ata ttg aca gga aac ccc atc cag agt tta gcc ctg gga 240
 Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly
 65 70 75 80
 gcc ttt tct gga cta tca agt tta cag aag ctg gtg gct gtg gag aca 288
 Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr
 85 90 95
 aat cta gca tct cta gag aac ttc ccc att gga cat ctc aaa act ttg 336
 Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu

100						105						110						
aaa	gaa	ctt	aat	gtg	gct	cac	aat	ctt	atc	caa	tct	ttc	aaa	tta	cct	384		
Lys	Glu	Leu	Asn	Val	Ala	His	Asn	Leu	Ile	Gln	Ser	Phe	Lys	Leu	Pro			
		115					120					125						
gag	tat	ttt	tct	aat	ctg	acc	aat	cta	gag	cac	ttg	gac	ctt	tcc	agc	432		
Glu	Tyr	Phe	Ser	Asn	Leu	Thr	Asn	Leu	Glu	His	Leu	Asp	Leu	Ser	Ser			
	130					135					140							
aac	aag	att	caa	agt	att	tat	tgc	aca	gac	ttg	cgg	gtt	cta	cat	caa	480		
Asn	Lys	Ile	Gln	Ser	Ile	Tyr	Cys	Thr	Asp	Leu	Arg	Val	Leu	His	Gln			
145					150					155					160			
atg	ccc	cta	ctc	aat	ctc	tct	tta	gac	ctg	tcc	ctg	aac	cct	atg	aac	528		
Met	Pro	Leu	Leu	Asn	Leu	Ser	Leu	Asp	Leu	Ser	Leu	Asn	Pro	Met	Asn			
				165					170					175				
ttt	atc	caa	cca	ggg	gca	ttt	aaa	gaa	att	agg	ctt	cat	aag	ctg	act	576		
Phe	Ile	Gln	Pro	Gly	Ala	Phe	Lys	Glu	Ile	Arg	Leu	His	Lys	Leu	Thr			
			180					185					190					
tta	aga	aat	aat	ttt	gat	agt	tta	aat	gta	atg	aaa	act	tgt	att	caa	624		
Leu	Arg	Asn	Asn	Phe	Asp	Ser	Leu	Asn	Val	Met	Lys	Thr	Cys	Ile	Gln			
		195					200					205						
ggg	ctg	gct	ggg	tta	gaa	gtc	cat	cgt	ttg	gtt	ctg	gga	gaa	ttt	aga	672		
Gly	Leu	Ala	Gly	Leu	Glu	Val	His	Arg	Leu	Val	Leu	Gly	Glu	Phe	Arg			
	210					215					220							
aat	gaa	gga	aac	ttg	gaa	aag	ttt	gac	aaa	tct	gct	cta	gag	ggc	ctg	720		
Asn	Glu	Gly	Asn	Leu	Glu	Lys	Phe	Asp	Lys	Ser	Ala	Leu	Glu	Gly	Leu			
225					230				235						240			
tgg	aat	ttg	acc	att	gaa	gaa	ttc	cga	tta	gca	tac	tta	gac	tac	tac	768		
Cys	Asn	Leu	Thr	Ile	Glu	Glu	Phe	Arg	Leu	Ala	Tyr	Leu	Asp	Tyr	Tyr			
				245				250						255				
ctc	gat	gat	att	att	gac	tta	ttt	aat	tgt	ttg	aca	aat	gtt	tct	tca	816		
Leu	Asp	Asp	Ile	Ile	Asp	Leu	Phe	Asn	Cys	Leu	Thr	Asn	Val	Ser	Ser			
			260					265					270					
ttt	tcc	ctg	gtg	agt	gtg	act	att	gaa	agg	gta	aaa	gac	ttt	tct	tat	864		
Phe	Ser	Leu	Val	Ser	Val	Thr	Ile	Glu	Arg	Val	Lys	Asp	Phe	Ser	Tyr			
		275				280						285						
aat	ttc	gga	tgg	caa	cat	tta	gaa	tta	gtt	aac	tgt	aaa	ttt	gga	cag	912		
Asn	Phe	Gly	Trp	Gln	His	Leu	Glu	Leu	Val	Asn	Cys	Lys	Phe	Gly	Gln			
	290					295					300							
ttt	ccc	aca	ttg	aaa	ctc	aaa	tct	ctc	aaa	agg	ctt	act	ttc	act	tcc	960		
Phe	Pro	Thr	Leu	Lys	Leu	Lys	Ser	Leu	Lys	Arg	Leu	Thr	Phe	Thr	Ser			
305					310				315						320			

aac	aaa	ggt	ggg	aat	gct	ttt	tca	gaa	gtt	gat	cta	cca	agc	ctt	gag	1008
Asn	Lys	Gly	Gly	Asn	Ala	Phe	Ser	Glu	Val	Asp	Leu	Pro	Ser	Leu	Glu	
				325					330					335		
ttt	cta	gat	ctc	agt	aga	aat	ggc	ttg	agt	ttc	aaa	ggt	tgc	tgt	tct	1056
Phe	Leu	Asp	Leu	Ser	Arg	Asn	Gly	Leu	Ser	Phe	Lys	Gly	Cys	Cys	Ser	
			340					345					350			
caa	agt	gat	ttt	ggg	aca	acc	agc	cta	aag	tat	tta	gat	ctg	agc	ttc	1104
Gln	Ser	Asp	Phe	Gly	Thr	Thr	Ser	Leu	Lys	Tyr	Leu	Asp	Leu	Ser	Phe	
		355					360					365				
aat	ggt	gtt	att	acc	atg	agt	tca	aac	ttc	ttg	ggc	tta	gaa	caa	cta	1152
Asn	Gly	Val	Ile	Thr	Met	Ser	Ser	Asn	Phe	Leu	Gly	Leu	Glu	Gln	Leu	
	370					375					380					
gaa	cat	ctg	gat	ttc	cag	cat	tcc	aat	ttg	aaa	caa	atg	agt	gag	ttt	1200
Glu	His	Leu	Asp	Phe	Gln	His	Ser	Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	
385					390					395					400	
tca	gta	ttc	cta	tca	ctc	aga	aac	ctc	att	tac	ctt	gac	att	tct	cat	1248
Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp	Ile	Ser	His	
				405					410					415		
acc	cac	acc	aga	gtt	gct	ttc	aat	ggc	atc	ttc	aat	ggc	ttg	tcc	agt	1296
Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly	Leu	Ser	Ser	
			420					425					430			
ctc	gaa	gtc	ttg	aaa	atg	gct	ggc	aat	tct	ttc	cag	gaa	aac	ttc	ctt	1344
Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Glu	Asn	Phe	Leu	
		435					440					445				
cca	gat	atc	ttc	aca	gag	ctg	aga	aac	ttg	acc	ttc	ctg	gac	ctc	tct	1392
Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu	Asp	Leu	Ser	
	450					455					460					
cag	tgt	caa	ctg	gag	cag	ttg	tct	cca	aca	gca	ttt	aac	tca	ctc	tcc	1440
Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn	Ser	Leu	Ser	
465					470					475					480	
agt	ctt	cag	gta	cta	aat	atg	agc	cac	aac	aac	ttc	ttt	tca	ttg	gat	1488
Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe	Ser	Leu	Asp	
				485					490					495		
acg	ttt	cct	tat	aag	tgt	ctg	aac	tcc	ctc	cag	gtt	ctt	gat	tac	agt	1536
Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu	Asp	Tyr	Ser	
			500					505					510			
ctc	aat	cac	ata	atg	act	tcc	aaa	aaa	cag	gaa	cta	cag	cat	ttt	cca	1584
Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln	His	Phe	Pro	
		515					520					525				
agt	agt	cta	gct	ttc	tta	aat	ctt	act	cag	aat	gac	ttt	gct	tgt	act	1632

Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe	Ala	Cys	Thr	
530						535					540					
tgt	gaa	cac	cag	agt	ttc	ctg	caa	tgg	atc	aag	gac	cag	agg	cag	ctc	1680
Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln	Arg	Gln	Leu	
545					550					555					560	
ttg	gtg	gaa	ggt	gaa	cga	atg	gaa	tgt	gca	aca	cct	tca	gat	aag	cag	1728
Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser	Asp	Lys	Gln	
				565					570					575		
ggc	atg	cct	gtg	ctg	agt	ttg	aat	atc	acc	tgt	cag	atg	aat	aag	acc	1776
Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met	Asn	Lys	Thr	
			580					585					590			
atc	att	ggt	gtg	tcg	gtc	ctc	agt	gtg	ctt	gta	gta	tct	gtt	gta	gca	1824
Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser	Val	Val	Ala	
		595					600					605				
gtt	ctg	gtc	tat	aag	ttc	tat	ttt	cac	ctg	atg	ctt	ctt	gct	ggc	tgc	1872
Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu	Met	Leu	Leu	Ala	Gly	Cys	
	610					615					620					
ata	aag	tat	ggt	aga	ggc	gaa	aac	atc	tat	gat	gcc	ttt	gtt	atc	tac	1920
Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	Ile	Tyr	Asp	Ala	Phe	Val	Ile	Tyr	
625					630					635					640	
tca	agc	cag	gat	gag	gac	tgg	gta	agg	aat	gag	cta	gta	aag	aat	tta	1968
Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn	Glu	Leu	Val	Lys	Asn	Leu	
				645					650					655		
gaa	gaa	ggg	gtg	cct	cca	ttt	cag	ctc	tgc	ctt	cac	tac	aga	gac	ttt	2016
Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys	Leu	His	Tyr	Arg	Asp	Phe	
			660				665					670				
att	ccc	ggt	gtg	gcc	att	gct	gcc	aac	atc	atc	cat	gaa	ggt	ttc	cat	2064
Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile	Ile	His	Glu	Gly	Phe	His	
		675				680						685				
aaa	agc	cga	aag	gtg	att	gtt	gtg	gtg	tcc	cag	cac	ttc	atc	cag	agc	2112
Lys	Ser	Arg	Lys	Val	Ile	Val	Val	Val	Ser	Gln	His	Phe	Ile	Gln	Ser	
	690					695					700					
cgc	tgg	tgt	atc	ttt	gaa	tat	gag	att	gct	cag	acc	tgg	cag	ttt	ctg	2160
Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	Ile	Ala	Gln	Thr	Trp	Gln	Phe	Leu	
705					710					715					720	
agc	agt	cgt	gct	ggc	atc	atc	ttc	att	gtc	ctg	cag	aag	gtg	gag	aag	2208
Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	Ile	Val	Leu	Gln	Lys	Val	Glu	Lys	
				725					730					735		
acc	ctg	ctc	agg	cag	cag	gtg	gag	ctg	tac	cgc	ctt	ctc	agc	agg	aac	2256
Thr	Leu	Leu	Arg	Gln	Gln	Val	Glu	Leu	Tyr	Arg	Leu	Leu	Ser	Arg	Asn	

740					745					750						
act	tac	ctg	gag	tgg	gag	gac	agt	gtc	ctg	ggg	cgg	cac	atc	ttc	tgg	2304
Thr	Tyr	Leu	Glu	Trp	Glu	Asp	Ser	Val	Leu	Gly	Arg	His	Ile	Phe	Trp	
		755					760					765				
aga	cga	ctc	aga	aaa	gcc	ctg	ctg	gat	ggg	aaa	tca	tgg	aat	cca	gaa	2352
Arg	Arg	Leu	Arg	Lys	Ala	Leu	Leu	Asp	Gly	Lys	Ser	Trp	Asn	Pro	Glu	
	770					775					780					
gga	aca	gtg	ggg	aca	gga	tgc	aat	tgg	cag	gaa	gca	aca	tct	atc	tga	2400
Gly	Thr	Val	Gly	Thr	Gly	Cys	Asn	Trp	Gln	Glu	Ala	Thr	Ser	Ile		
785					790					795						

<210> 8
 <211> 799
 <212> PRT
 <213> Unknown

<400> 8																
Met	Glu	Leu	Asn	Phe	Tyr	Lys	Ile	Pro	Asp	Asn	Leu	Pro	Phe	Ser	Thr	
				5					10					15		
Lys	Asn	Leu	Asp	Leu	Ser	Phe	Asn	Pro	Leu	Arg	His	Leu	Gly	Ser	Tyr	
			20					25					30			
Ser	Phe	Phe	Ser	Phe	Pro	Glu	Leu	Gln	Val	Leu	Asp	Leu	Ser	Arg	Cys	
		35					40					45				
Glu	Ile	Gln	Thr	Ile	Glu	Asp	Gly	Ala	Tyr	Gln	Ser	Leu	Ser	His	Leu	
	50					55					60					
Ser	Thr	Leu	Ile	Leu	Thr	Gly	Asn	Pro	Ile	Gln	Ser	Leu	Ala	Leu	Gly	
65					70					75					80	
Ala	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Lys	Leu	Val	Ala	Val	Glu	Thr	
				85					90					95		
Asn	Leu	Ala	Ser	Leu	Glu	Asn	Phe	Pro	Ile	Gly	His	Leu	Lys	Thr	Leu	
			100					105					110			
Lys	Glu	Leu	Asn	Val	Ala	His	Asn	Leu	Ile	Gln	Ser	Phe	Lys	Leu	Pro	
		115					120					125				
Glu	Tyr	Phe	Ser	Asn	Leu	Thr	Asn	Leu	Glu	His	Leu	Asp	Leu	Ser	Ser	
	130					135					140					
Asn	Lys	Ile	Gln	Ser	Ile	Tyr	Cys	Thr	Asp	Leu	Arg	Val	Leu	His	Gln	
145					150					155					160	
Met	Pro	Leu	Leu	Asn	Leu	Ser	Leu	Asp	Leu	Ser	Leu	Asn	Pro	Met	Asn	
				165					170					175		

Phe	Ile	Gln	Pro	Gly	Ala	Phe	Lys	Glu	Ile	Arg	Leu	His	Lys	Leu	Thr	180	185	190
Leu	Arg	Asn	Asn	Phe	Asp	Ser	Leu	Asn	Val	Met	Lys	Thr	Cys	Ile	Gln	195	200	205
Gly	Leu	Ala	Gly	Leu	Glu	Val	His	Arg	Leu	Val	Leu	Gly	Glu	Phe	Arg	210	215	220
Asn	Glu	Gly	Asn	Leu	Glu	Lys	Phe	Asp	Lys	Ser	Ala	Leu	Glu	Gly	Leu	225	230	235
Cys	Asn	Leu	Thr	Ile	Glu	Glu	Phe	Arg	Leu	Ala	Tyr	Leu	Asp	Tyr	Tyr	245	250	255
Leu	Asp	Asp	Ile	Ile	Asp	Leu	Phe	Asn	Cys	Leu	Thr	Asn	Val	Ser	Ser	260	265	270
Phe	Ser	Leu	Val	Ser	Val	Thr	Ile	Glu	Arg	Val	Lys	Asp	Phe	Ser	Tyr	275	280	285
Asn	Phe	Gly	Trp	Gln	His	Leu	Glu	Leu	Val	Asn	Cys	Lys	Phe	Gly	Gln	290	295	300
Phe	Pro	Thr	Leu	Lys	Leu	Lys	Ser	Leu	Lys	Arg	Leu	Thr	Phe	Thr	Ser	305	310	315
Asn	Lys	Gly	Gly	Asn	Ala	Phe	Ser	Glu	Val	Asp	Leu	Pro	Ser	Leu	Glu	325	330	335
Phe	Leu	Asp	Leu	Ser	Arg	Asn	Gly	Leu	Ser	Phe	Lys	Gly	Cys	Cys	Ser	340	345	350
Gln	Ser	Asp	Phe	Gly	Thr	Thr	Ser	Leu	Lys	Tyr	Leu	Asp	Leu	Ser	Phe	355	360	365
Asn	Gly	Val	Ile	Thr	Met	Ser	Ser	Asn	Phe	Leu	Gly	Leu	Glu	Gln	Leu	370	375	380
Glu	His	Leu	Asp	Phe	Gln	His	Ser	Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	385	390	395
Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp	Ile	Ser	His	405	410	415
Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly	Leu	Ser	Ser	420	425	430
Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Glu	Asn	Phe	Leu	435	440	445
Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu	Asp	Leu	Ser	450	455	460

Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn	Ser	Leu	Ser	
465					470					475					480	
Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe	Ser	Leu	Asp	
				485					490					495		
Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu	Asp	Tyr	Ser	
			500					505					510			
Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln	His	Phe	Pro	
		515					520					525				
Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe	Ala	Cys	Thr	
	530					535					540					
Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln	Arg	Gln	Leu	
545					550					555					560	
Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser	Asp	Lys	Gln	
				565					570					575		
Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met	Asn	Lys	Thr	
			580					585					590			
Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser	Val	Val	Ala	
		595					600					605				
Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu	Met	Leu	Leu	Ala	Gly	Cys	
	610					615					620					
Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	Ile	Tyr	Asp	Ala	Phe	Val	Ile	Tyr	
625					630					635					640	
Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn	Glu	Leu	Val	Lys	Asn	Leu	
				645					650					655		
Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys	Leu	His	Tyr	Arg	Asp	Phe	
			660					665					670			
Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile	Ile	His	Glu	Gly	Phe	His	
		675					680					685				
Lys	Ser	Arg	Lys	Val	Ile	Val	Val	Val	Ser	Gln	His	Phe	Ile	Gln	Ser	
	690					695					700					
Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	Ile	Ala	Gln	Thr	Trp	Gln	Phe	Leu	
705					710					715					720	
Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	Ile	Val	Leu	Gln	Lys	Val	Glu	Lys	
				725					730					735		
Thr	Leu	Leu	Arg	Gln	Gln	Val	Glu	Leu	Tyr	Arg	Leu	Leu	Ser	Arg	Asn	
			740					745					750			

Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp
755 760 765

Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu
770 775 780

Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile
785 790 795

<210> 9
<211> 1275
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (1)..(1095)

<220> 9
tgt tgg gat gtt ttt gag gga ctt tct cat ctt caa gtt ctg tat ttg 48
Cys Trp Asp Val Phe Glu Gly Leu Ser His Leu Gln Val Leu Tyr Leu
1 5 10 15

aat cat aac tat ctt aat tcc ctt cca cca gga gta ttt agc cat ctg 96
Asn His Asn Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu
20 25 30

act gca tta agg gga cta agc ctc aac tcc aac agg ctg aca gtt ctt 144
Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu
35 40 45

tct cac aat gat tta cct gct aat tta gag atc ctg gac ata tcc agg 192
Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg
50 55 60

aac cag ctc cta gct cct aat cct gat gta ttt gta tca ctt agt gtc 240
Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val
65 70 75 80

ttg gat ata act cat aac aag ttc att tgt gaa tgt gaa ctt agc act 288
Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr
85 90 95

ttt atc aat tgg ctt aat cac acc aat gtc act ata gct ggg cct cct 336
Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro
100 105 110

gca gac ata tat tgt gtg tac cct gac tcg ttc tct ggg gtt tcc ctc	384
Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu	
115 120 125	
ttc tct ctt tcc acg gaa ggt tgt gat gaa gag gaa gtc tta aag tcc	432
Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser	
130 135 140	
cta aag ttc tcc ctt ttc att gta tgc act gtc act ctg act ctg ttc	480
Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe	
145 150 155 160	
ctc atg acc atc ctc aca gtc aca aag ttc cgg ggc ttc tgt ttt atc	528
Leu Met Thr Ile Leu Thr Val Thr Lys Phe Arg Gly Phe Cys Phe Ile	
165 170 175	
tgt tat aag aca gcc cag aga ctg gtg ttc aag gac cat ccc cag ggc	576
Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys Asp His Pro Gln Gly	
180 185 190	
aca gaa cct gat atg tac aaa tat gat gcc tat ttg tgc ttc agc agc	624
Thr Glu Pro Asp Met Tyr Lys Tyr Asp Ala Tyr Leu Cys Phe Ser Ser	
195 200 205	
aaa gac ttc aca tgg gtg cag aat gct ttg ctc aaa cac ctg gac act	672
Lys Asp Phe Thr Trp Val Gln Asn Ala Leu Leu Lys His Leu Asp Thr	
210 215 220	
caa tac agt gac caa aac aga ttc aac ctg tgc ttt gaa gaa aga gac	720
Gln Tyr Ser Asp Gln Asn Arg Phe Asn Leu Cys Phe Glu Glu Arg Asp	
225 230 235 240	
ttt gtc cca gga gaa aac cgc att gcc aat atc cag gat gcc atc tgg	768
Phe Val Pro Gly Glu Asn Arg Ile Ala Asn Ile Gln Asp Ala Ile Trp	
245 250 255	
aac agt aga aag atc gtt tgt ctt gtg agc aga cac ttc ctt aga gat	816
Asn Ser Arg Lys Ile Val Cys Leu Val Ser Arg His Phe Leu Arg Asp	
260 265 270	
ggc tgg tgc ctt gaa gcc ttc agt tat gcc cag ggc agg tgc tta tct	864
Gly Trp Cys Leu Glu Ala Phe Ser Tyr Ala Gln Gly Arg Cys Leu Ser	
275 280 285	
gac ctt aac agt gct ctc atc atg gtg gtg gtt ggg tcc ttg tcc cag	912
Asp Leu Asn Ser Ala Leu Ile Met Val Val Val Gly Ser Leu Ser Gln	
290 295 300	
tac cag ttg atg aaa cat caa tcc atc aga ggc ttt gta cag aaa cag	960
Tyr Gln Leu Met Lys His Gln Ser Ile Arg Gly Phe Val Gln Lys Gln	
305 310 315 320	
cag tat ttg agg tgg cct gag gat ctc cag gat gtt ggc tgg ttt ctt	1008
Gln Tyr Leu Arg Trp Pro Glu Asp Leu Gln Asp Val Gly Trp Phe Leu	

	325		330		335	
cat aaa ctc tct caa cag ata cta aag aaa gaa aag gaa aag aag aaa.						1056
His Lys Leu Ser Gln Gln Ile Leu Lys Lys Glu Lys Glu Lys Lys Lys	340		345		350	
gac aat aac att ccg ttg caa act gta gca acc atc tcc taatcaaagg						1105
Asp Asn Asn Ile Pro Leu Gln Thr Val Ala Thr Ile Ser	355		360		365	
agcaatttcc aacttatctc aagccacaaa taactcttca ctttgtatatt gcaccaagtt						1165
atcatttttg ggtcctctct ggaggttttt ttttctttt tgctactatg aaaacaacat						1225
aaatctctca attttcgtat caaaaaaaaa aaaaaaaaaa tggcggccgc						1275

<210> 10
 <211> 365
 <212> PRT
 <213> Unknown

<400> 10	
Cys Trp Asp Val Phe Glu Gly Leu Ser His Leu Gln Val Leu Tyr Leu	
	5 10 15
Asn His Asn Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu	
	20 25 30
Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu	
	35 40 45
Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg	
	50 55 60
Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val	
	65 70 75 80
Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr	
	85 90 95
Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro	
	100 105 110
Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu	
	115 120 125
Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser	
	130 135 140
Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe	
	145 150 155 160

Leu	Met	Thr	Ile	Leu	Thr	Val	Thr	Lys	Phe	Arg	Gly	Phe	Cys	Phe	Ile
				165					170					175	
Cys	Tyr	Lys	Thr	Ala	Gln	Arg	Leu	Val	Phe	Lys	Asp	His	Pro	Gln	Gly
			180					185					190		
Thr	Glu	Pro	Asp	Met	Tyr	Lys	Tyr	Asp	Ala	Tyr	Leu	Cys	Phe	Ser	Ser
		195					200					205			
Lys	Asp	Phe	Thr	Trp	Val	Gln	Asn	Ala	Leu	Leu	Lys	His	Leu	Asp	Thr
	210					215					220				
Gln	Tyr	Ser	Asp	Gln	Asn	Arg	Phe	Asn	Leu	Cys	Phe	Glu	Glu	Arg	Asp
225					230					235					240
Phe	Val	Pro	Gly	Glu	Asn	Arg	Ile	Ala	Asn	Ile	Gln	Asp	Ala	Ile	Trp
				245					250					255	
Asn	Ser	Arg	Lys	Ile	Val	Cys	Leu	Val	Ser	Arg	His	Phe	Leu	Arg	Asp
			260					265					270		
Gly	Trp	Cys	Leu	Glu	Ala	Phe	Ser	Tyr	Ala	Gln	Gly	Arg	Cys	Leu	Ser
		275					280					285			
Asp	Leu	Asn	Ser	Ala	Leu	Ile	Met	Val	Val	Val	Gly	Ser	Leu	Ser	Gln
	290					295					300				
Tyr	Gln	Leu	Met	Lys	His	Gln	Ser	Ile	Arg	Gly	Phe	Val	Gln	Lys	Gln
305					310					315					320
Gln	Tyr	Leu	Arg	Trp	Pro	Glu	Asp	Leu	Gln	Asp	Val	Gly	Trp	Phe	Leu
				325					330					335	
His	Lys	Leu	Ser	Gln	Gln	Ile	Leu	Lys	Lys	Glu	Lys	Glu	Lys	Lys	Lys
			340					345					350		
Asp	Asn	Asn	Ile	Pro	Leu	Gln	Thr	Val	Ala	Thr	Ile	Ser			
		355					360					365			

<210> 11

<211> 3138

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (1)..(3135)

<220>

<221> mat_peptide
 <222> (67)..(3135)

<400> 11

atg tgg aca ctg aag aga cta att ctt atc ctt ttt aac ata atc cta	48
Met Trp Thr Leu Lys Arg Leu Ile Leu Ile Leu Phe Asn Ile Ile Leu	
-20 -15 -10	
att tcc aaa ctc ctt ggg gct aga tgg ttt cct aaa act ctg ccc tgt	96
Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys Thr Leu Pro Cys	
-5 -1 1 5 10	
gat gtc act ctg gat gtt cca aag aac cat gtg atc gtg gac tgc aca	144
Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile Val Asp Cys Thr	
15 20 25	
gac aag cat ttg aca gaa att cct gga ggt att ccc acg aac acc acg	192
Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro Thr Asn Thr Thr	
30 35 40	
aac ctc acc ctc acc att aac cac ata cca gac atc tcc cca gcg tcc	240
Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile Ser Pro Ala Ser	
45 50 55	
ttt cac aga ctg gac cat ctg gta gag atc gat ttc aga tgc aac tgt	288
Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe Arg Cys Asn Cys	
60 65 70	
gta cct att cca ctg ggg tca aaa aac aac atg tgc atc aag agg ctg	336
Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu	
75 80 85 90	
cag att aaa ccc aga agc ttt agt gga ctc act tat tta aaa tcc ctt	384
Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu	
95 100 105	
tac ctg gat gga aac cag cta cta gag ata ccg cag ggc ctc ccg cct	432
Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro	
110 115 120	
agc tta cag ctt ctc agc ctt gag gcc aac aac atc ttt tcc atc aga	480
Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg	
125 130 135	
aaa gag aat cta aca gaa ctg gcc aac ata gaa ata ctc tac ctg ggc	528
Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly	
140 145 150	
caa aac tgt tat tat cga aat cct tgt tat gtt tca tat tca ata gag	576
Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile Glu	
155 160 165 170	
aaa gat gcc ttc cta aac ttg aca aag tta aaa gtg ctc tcc ctg aaa	624

Lys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Lys	Leu	Lys	Val	Leu	Ser	Leu	Lys	
				175					180					185		
gat	aac	aat	gtc	aca	gcc	gtc	cct	act	gtt	ttg	cca	tct	act	tta	aca	672
Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser	Thr	Leu	Thr	
			190					195					200			
gaa	cta	tat	ctc	tac	aac	aac	atg	att	gca	aaa	atc	caa	gaa	gat	gat	720
Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile	Gln	Glu	Asp	Asp	
		205					210					215				
ttt	aat	aac	ctc	aac	caa	tta	caa	att	ctt	gac	cta	agt	gga	aat	tgc	768
Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp	Leu	Ser	Gly	Asn	Cys	
	220					225					230					
cct	cgt	tgt	tat	aat	gcc	cca	ttt	cct	tgt	gcg	ccg	tgt	aaa	aat	aat	816
Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	Ala	Pro	Cys	Lys	Asn	Asn	
235					240					245					250	
tct	ccc	cta	cag	atc	cct	gta	aat	gct	ttt	gat	gcg	ctg	aca	gaa	tta	864
Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	Phe	Asp	Ala	Leu	Thr	Glu	Leu	
				255					260					265		
aaa	gtt	tta	cgt	cta	cac	agt	aac	tct	ctt	cag	cat	gtg	ccc	cca	aga	912
Lys	Val	Leu	Arg	Leu	His	Ser	Asn	Ser	Leu	Gln	His	Val	Pro	Pro	Arg	
			270					275					280			
tgg	ttt	aag	aac	atc	aac	aaa	ctc	cag	gaa	ctg	gat	ctg	tcc	caa	aac	960
Trp	Phe	Lys	Asn	Ile	Asn	Lys	Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn	
		285					290					295				
ttc	ttg	gcc	aaa	gaa	att	ggg	gat	gct	aaa	ttt	ctg	cat	ttt	ctc	ccc	1008
Phe	Leu	Ala	Lys	Glu	Ile	Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	
	300					305					310					
agc	ctc	atc	caa	ttg	gat	ctg	tct	ttc	aat	ttt	gaa	ctt	cag	gtc	tat	1056
Ser	Leu	Ile	Gln	Leu	Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	
315					320					325					330	
cgt	gca	tct	atg	aat	cta	tca	caa	gca	ttt	tct	tca	ctg	aaa	agc	ctg	1104
Arg	Ala	Ser	Met	Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	
				335					340					345		
aaa	att	ctg	cgg	atc	aga	gga	tat	gtc	ttt	aaa	gag	ttg	aaa	agc	ttt	1152
Lys	Ile	Leu	Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	
			350					355					360			
aac	ctc	tcg	cca	tta	cat	aat	ctt	caa	aat	ctt	gaa	gtt	ctt	gat	ctt	1200
Asn	Leu	Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	
		365					370					375				
ggc	act	aac	ttt	ata	aaa	att	gct	aac	ctc	agc	atg	ttt	aaa	caa	ttt	1248
Gly	Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
	380					385					390					

aaa	aga	ctg	aaa	gtc	ata	gat	ctt	tca	gtg	aat	aaa	ata	tca	cct	tca	1296
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	Ser	
395					400					405					410	
gga	gat	tca	agt	gaa	gtt	ggc	ttc	tgc	tca	aat	gcc	aga	act	tct	gta	1344
Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	Ser	Val	
				415					420					425		
gaa	agt	tat	gaa	ccc	cag	gtc	ctg	gaa	caa	tta	cat	tat	ttc	aga	tat	1392
Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	Phe	Arg	Tyr	
			430					435					440			
gat	aag	tat	gca	agg	agt	tgc	aga	ttc	aaa	aac	aaa	gag	gct	tct	ttc	1440
Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	Glu	Ala	Ser	Phe	
		445					450					455				
atg	tct	gtt	aat	gaa	agc	tgc	tac	aag	tat	ggg	cag	acc	ttg	gat	cta	1488
Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	Gln	Thr	Leu	Asp	Leu	
	460					465					470					
agt	aaa	aat	agt	ata	ttt	ttt	gtc	aag	tcc	tct	gat	ttt	cag	cat	ctt	1536
Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	Ser	Asp	Phe	Gln	His	Leu	
475				480						485					490	
tct	ttc	ctc	aaa	tgc	ctg	aat	ctg	tca	gga	aat	ctc	att	agc	caa	act	1584
Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Ile	Ser	Gln	Thr	
				495					500					505		
ctt	aat	ggc	agt	gaa	ttc	caa	cct	tta	gca	gag	ctg	aga	tat	ttg	gac	1632
Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	
			510					515					520			
ttc	tcc	aac	aac	cgg	ctt	gat	tta	ctc	cat	tca	aca	gca	ttt	gaa	gag	1680
Phe	Ser	Asn	Asn	Arg	Leu	Asp	Leu	Leu	His	Ser	Thr	Ala	Phe	Glu	Glu	
		525					530					535				
ctt	cac	aaa	ctg	gaa	gtt	ctg	gat	ata	agc	agt	aat	agc	cat	tat	ttt	1728
Leu	His	Lys	Leu	Glu	Val	Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe	
	540					545					550					
caa	tca	gaa	gga	att	act	cat	atg	cta	aac	ttt	acc	aag	aac	cta	aag	1776
Gln	Ser	Glu	Gly	Ile	Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys	
555					560					565					570	
gtt	ctg	cag	aaa	ctg	atg	atg	aac	gac	aat	gac	atc	tct	tcc	tcc	acc	1824
Val	Leu	Gln	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	Ser	Ser	Ser	Thr	
				575					580					585		
agc	agg	acc	atg	gag	agt	gag	tct	ctt	aga	act	ctg	gaa	ttc	aga	gga	1872
Ser	Arg	Thr	Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly	
			590					595					600			

aat Asn	cac His	tta Leu	gat Asp	gtt Val	tta Leu	tgg Trp	aga Arg	gaa Glu	ggt Gly	gat Asp	aac Asn	aga Arg	tac Tyr	tta Leu	caa Gln	1920
		605					610					615				
tta Leu	ttc Phe	aag Lys	aat Asn	ctg Leu	cta Leu	aaa Lys	tta Leu	gag Glu	gaa Glu	tta Leu	gac Asp	atc Ile	tct Ser	aaa Lys	aat Asn	1968
	620					625					630					
tcc Ser	cta Leu	agt Ser	ttc Phe	ttg Leu	cct Pro	tct Ser	gga Gly	gtt Val	ttt Phe	gat Asp	ggt Gly	atg Met	cct Pro	cca Pro	aat Asn	2016
	635				640					645					650	
cta Leu	aag Lys	aat Asn	ctc Leu	tct Ser	ttg Leu	gcc Ala	aaa Lys	aat Asn	ggg Gly	ctc Leu	aaa Lys	tct Ser	ttc Phe	agt Ser	tgg Trp	2064
				655					660					665		
aag Lys	aaa Lys	ctc Leu	cag Gln	tgt Cys	cta Leu	aag Lys	aac Asn	ctg Leu	gaa Glu	act Thr	ttg Leu	gac Asp	ctc Leu	agc Ser	cac His	2112
			670					675					680			
aaa Asn	caa Gln	ctg Leu	acc Thr	act Thr	gtc Val	cct Pro	gag Glu	aga Arg	tta Leu	tcc Ser	aac Asn	tgt Cys	tcc Ser	aga Arg	agc Ser	2160
		685					690					695				
ctc Leu	aag Lys	aat Asn	ctg Leu	att Ile	ctt Leu	aag Lys	aat Asn	aat Asn	caa Gln	atc Ile	agg Arg	agt Ser	ctg Leu	acg Thr	aag Lys	2208
	700					705					710					
tat Tyr	ttt Phe	cta Leu	caa Gln	gat Asp	gcc Ala	ttc Phe	cag Gln	ttg Leu	cga Arg	tat Tyr	ctg Leu	gat Asp	ctc Leu	agc Ser	tca Ser	2256
	715				720				725						730	
aat Asn	aaa Lys	atc Ile	cag Gln	atg Met	atc Ile	caa Gln	aag Lys	acc Thr	agc Ser	ttc Phe	cca Pro	gaa Glu	aat Asn	gtc Val	ctc Leu	2304
				735				740						745		
aac Asn	aat Asn	ctg Leu	aag Lys	atg Met	ttg Leu	ctt Leu	ttg Leu	cat His	cat His	aat Asn	cgg Arg	ttt Phe	ctg Leu	tgc Cys	acc Thr	2352
		750					755						760			
tgt Cys	gat Asp	gct Ala	gtg Val	tgg Trp	ttt Phe	gtc Val	tgg Trp	tgg Trp	gtt Val	aac Asn	cat His	acg Thr	gag Glu	gtg Val	act Thr	2400
		765					770					775				
att Ile	cct Pro	tac Tyr	ctg Leu	gcc Ala	aca Thr	gat Asp	gtg Val	act Thr	tgt Cys	gtg Val	ggg Gly	cca Pro	gga Gly	gca Ala	cac His	2448
	780					785					790					
aag Lys	ggc Gly	caa Gln	agt Ser	gtg Val	atc Ile	tcc Ser	ctg Leu	gat Asp	ctg Leu	tac Tyr	acc Thr	tgt Cys	gag Glu	tta Leu	gat Asp	2496
	795				800					805					810	
ctg Leu	act Thr	aac Asn	ctg Leu	att Ile	ctg Leu	ttc Phe	tca Ser	ctt Leu	tcc Ser	ata Ile	tct Ser	gta Val	tct Ser	ctc Leu	ttt Phe	2544

815								820				825					
ctc	atg	gtg	atg	atg	aca	gca	agt	cac	ctc	tat	ttc	tgg	gat	gtg	tgg	2592	
Leu	Met	Val	Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp		
830								835				840					
tat	att	tac	cat	ttc	tgt	aag	gcc	aag	ata	aag	ggg	tat	cag	cgt	cta	2640	
Tyr	Ile	Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu		
845								850				855					
ata	tca	cca	gac	tgt	tgc	tat	gat	gct	ttt	att	gtg	tat	gac	act	aaa	2688	
Ile	Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys		
860								865				870					
gac	cca	gct	gtg	acc	gag	tgg	gtt	ttg	gct	gag	ctg	gtg	gcc	aaa	ctg	2736	
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	Leu		
875								880				885				890	
gaa	gac	cca	aga	gag	aaa	cat	ttt	aat	tta	tgt	ctc	gag	gaa	agg	gac	2784	
Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu	Arg	Asp		
895								900				905					
tgg	tta	cca	ggg	cag	cca	gtt	ctg	gaa	aac	ctt	tcc	cag	agc	ata	cag	2832	
Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	Ser	Ile	Gln		
910								915				920					
ctc	agc	aaa	aag	aca	gtg	ttt	gtg	atg	aca	gac	aag	tat	gca	aag	act	2880	
Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	Tyr	Ala	Lys	Thr		
925								930				935					
gaa	aat	ttt	aag	ata	gca	ttt	tac	ttg	tcc	cat	cag	agg	ctc	atg	gat	2928	
Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	Gln	Arg	Leu	Met	Asp		
940								945				950					
gaa	aaa	gtt	gat	gtg	att	atc	ttg	ata	ttt	ctt	gag	aag	ccc	ttt	cag	2976	
Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	Leu	Glu	Lys	Pro	Phe	Gln		
955								960				965				970	
aag	tcc	aag	ttc	ctc	cag	ctc	cgg	aaa	agg	ctc	tgt	ggg	agt	tct	gtc	3024	
Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	Leu	Cys	Gly	Ser	Ser	Val		
975								980				985					
ctt	gag	tgg	cca	aca	aac	ccg	caa	gct	cac	cca	tac	ttc	tgg	cag	tgt	3072	
Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys		
990								995				1000					
cta	aag	aac	gcc	ctg	gcc	aca	gac	aat	cat	gtg	gcc	tat	agt	cag	gtg	3120	
Leu	Lys	Asn	Ala	Leu	Ala	Thr	Asp	Asn	His	Val	Ala	Tyr	Ser	Gln	Val		
1005								1010				1015					
ttc	aag	gaa	acg	gtc	tag											3138	
Phe	Lys	Glu	Thr	Val													
1020																	

<210> 12
<211> 1045
<212> PRT
<213> Unknown

<400> 12

Met Trp Thr Leu Lys Arg Leu Ile Leu Ile Leu Phe Asn Ile Ile Leu
-20 -15 -10

Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys Thr Leu Pro Cys
-5 -1 1 5 10

Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile Val Asp Cys Thr
15 20 25

Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro Thr Asn Thr Thr
30 35 40

Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile Ser Pro Ala Ser
45 50 55

Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe Arg Cys Asn Cys
60 65 70

Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu
75 80 85 90

Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu
95 100 105

Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro
110 115 120

Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg
125 130 135

Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
140 145 150

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile Glu
155 160 165 170

Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser Leu Lys
175 180 185

Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser Thr Leu Thr
190 195 200

Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile Gln Glu Asp Asp
205 210 215

Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu Ser Gly Asn Cys

220					225					230					
Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	Ala	Pro	Cys	Lys	Asn	Asn
235					240					245					250
Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	Phe	Asp	Ala	Leu	Thr	Glu	Leu
				255					260					265	
Lys	Val	Leu	Arg	Leu	His	Ser	Asn	Ser	Leu	Gln	His	Val	Pro	Pro	Arg
			270					275					280		
Trp	Phe	Lys	Asn	Ile	Asn	Lys	Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn
		285					290					295			
Phe	Leu	Ala	Lys	Glu	Ile	Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro
	300					305					310				
Ser	Leu	Ile	Gln	Leu	Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr
315					320					325					330
Arg	Ala	Ser	Met	Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu
				335					340					345	
Lys	Ile	Leu	Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe
			350					355					360		
Asn	Leu	Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu
		365					370					375			
Gly	Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe
	380					385					390				
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	Ser
395					400					405					410
Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	Ser	Val
				415					420					425	
Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	Phe	Arg	Tyr
			430					435					440		
Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	Glu	Ala	Ser	Phe
		445					450					455			
Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	Gln	Thr	Leu	Asp	Leu
	460					465					470				
Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	Ser	Asp	Phe	Gln	His	Leu
475					480					485					490
Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Ile	Ser	Gln	Thr
				495					500					505	

Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp
			510					515					520		
Phe	Ser	Asn	Asn	Arg	Leu	Asp	Leu	Leu	His	Ser	Thr	Ala	Phe	Glu	Glu
		525					530					535			
Leu	His	Lys	Leu	Glu	Val	Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe
	540					545					550				
Gln	Ser	Glu	Gly	Ile	Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys
555					560					565					570
Val	Leu	Gln	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	Ser	Ser	Ser	Thr
				575					580					585	
Ser	Arg	Thr	Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly
			590					595					600		
Asn	His	Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn	Arg	Tyr	Leu	Gln
		605					610					615			
Leu	Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp	Ile	Ser	Lys	Asn
	620					625					630				
Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly	Met	Pro	Pro	Asn
635					640					645					650
Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	Ser	Phe	Ser	Trp
				655					660					665	
Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp	Leu	Ser	His
			670					675					680		
Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn	Cys	Ser	Arg	Ser
		685					690					695			
Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	Arg	Ser	Leu	Thr	Lys
	700					705					710				
Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Ser
715					720					725					730
Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	Ser	Phe	Pro	Glu	Asn	Val	Leu
				735					740					745	
Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu	His	His	Asn	Arg	Phe	Leu	Cys	Thr
			750					755					760		
Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr
		765					770					775			
Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His
	780					785					790				

Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp
 795 800 805 810
 Leu Thr Asn Leu Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe
 815 820 825
 Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp
 830 835 840
 Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu
 845 850 855
 Ile Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys
 860 865 870
 Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys Leu
 875 880 885 890
 Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu Arg Asp
 895 900 905
 Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln Ser Ile Gln
 910 915 920
 Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys Tyr Ala Lys Thr
 925 930 935
 Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln Arg Leu Met Asp
 940 945 950
 Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu Lys Pro Phe Gln
 955 960 965 970
 Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys Gly Ser Ser Val
 975 980 985
 Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro Tyr Phe Trp Gln Cys
 990 995 1000
 Leu Lys Asn Ala Leu Ala Thr Asp Asn His Val Ala Tyr Ser Gln Val
 1005 1010 1015
 Phe Lys Glu Thr Val
 1020

<210> 13

<211> 180

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised

Mus musculus

<220>

<221> CDS

<222> (1)..(177)

<400> 13

ctt	gga	aaa	cct	ctt	cag	aag	tct	aag	ttt	ctt	cag	ctc	agg	aag	aga	48
Leu	Gly	Lys	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	
1				5					10					15		

ctc	tgc	agg	agc	tct	gtc	ctt	gag	tgg	cct	gca	aat	cca	cag	gct	cac	96
Leu	Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	
			20					25					30			

cca	tac	ttc	tgg	cag	tgc	ctg	aaa	aat	gcc	ctg	acc	aca	gac	aat	cat	144
Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	
		35					40					45				

gtg	gct	tat	agt	caa	atg	ttc	aag	gaa	aca	gtc	tag					180
Val	Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val						
	50					55										

<210> 14

<211> 59

<212> PRT

<213> Unknown

<400> 14

Leu	Gly	Lys	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg
1				5					10					15	

Leu	Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His
			20					25					30		

Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His
		35					40					45			

Val	Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val					
	50					55									

<210> 15

<211> 990

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (2) .. (988)

<400> 15

g	aat	tcc	aga	ctt	ata	aac	ttg	aaa	aat	ctc	tat	ttg	gcc	tg	aac	tgc	49
Asn	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn	Cys		
1				5				10					15				
tat	ttt	aac	aaa	gtt	tgc	gag	aaa	act	aac	ata	gaa	gat	gga	gta	ttt	97	
Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly	Val	Phe		
		20						25					30				
gaa	acg	ctg	aca	aat	ttg	gag	ttg	cta	tca	cta	tct	ttc	aat	tct	ctt	145	
Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe	Asn	Ser	Leu		
		35					40					45					
tca	cat	gtg	cca	ccc	aaa	ctg	cca	agc	tcc	cta	cgc	aaa	ctt	ttt	ctg	193	
Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg	Lys	Leu	Phe	Leu		
	50					55					60						
agc	aac	acc	cag	atc	aaa	tac	att	agt	gaa	gaa	gat	ttc	aag	gga	ttg	241	
Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu	Asp	Phe	Lys	Gly	Leu		
65					70					75					80		
ata	aat	tta	aca	tta	cta	gat	tta	agc	ggg	aac	tgt	ccg	agg	tgc	ttc	289	
Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Phe		
				85					90					95			
aat	gcc	cca	ttt	cca	tgc	gtg	cct	tgt	gat	ggg	ggg	gct	tca	att	aat	337	
Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys	Asp	Gly	Gly	Ala	Ser	Ile	Asn		
			100					105					110				
ata	gat	cgt	ttt	gct	ttt	caa	aac	ttg	acc	caa	ctt	cga	tac	cta	aac	385	
Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn	Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn		
		115					120					125					
ctc	tct	agc	act	tcc	ctc	agg	aag	att	aat	gct	gcc	tg	ttt	aaa	aat	433	
Leu	Ser	Ser	Thr	Ser	Leu	Arg	Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn		
	130					135					140						
atg	cct	cat	ctg	aag	gtg	ctg	gat	ctt	gaa	ttc	aac	tat	tta	gtg	gga	481	
Met	Pro	His	Leu	Lys	Val	Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly		
145					150					155					160		
gaa	ata	gcc	tct	ggg	gca	ttt	tta	acg	atg	ctg	ccc	cgc	tta	gaa	ata	529	
Glu	Ile	Ala	Ser	Gly	Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile		
				165					170					175			
ctt	gac	ttg	tct	ttt	aac	tat	ata	aag	ggg	agt	tat	cca	cag	cat	att	577	
Leu	Asp	Leu	Ser	Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile		
		180						185					190				
aat	att	tcc	aga	aac	ttc	tct	aaa	ctt	ttg	tct	cta	cgg	gca	ttg	cat	625	
Asn	Ile	Ser	Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His		

195					200					205						
tta	aga	ggg	tat	gtg	ttc	cag	gaa	ctc	aga	gaa	gat	gat	ttc	cag	ccc	673
Leu	Arg	Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	
	210					215					220					
ctg	atg	cag	ctt	cca	aac	tta	tcg	act	atc	aac	ttg	ggg	att	aat	ttt	721
Leu	Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	
	225				230					235					240	
att	aag	caa	atc	gat	ttc	aaa	ctt	ttc	caa	aat	ttc	tcc	aat	ctg	gaa	769
Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	Glu	
				245					250					255		
att	att	tac	ttg	tca	gaa	aac	aga	ata	tca	ccg	ttg	gta	aaa	gat	acc	817
Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	Asp	Thr	
			260					265					270			
cgg	cag	agt	tat	gca	aat	agt	tcc	tct	ttt	caa	cgt	cat	atc	cgg	aaa	865
Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	Ile	Arg	Lys	
		275					280					285				
cga	cgc	tca	aca	gat	ttt	gag	ttt	gac	cca	cat	tcg	aac	ttt	tat	cat	913
Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	Asn	Phe	Tyr	His	
		290				295					300					
ttc	acc	cgt	cct	tta	ata	aag	cca	caa	tgt	gct	gct	tat	gga	aaa	gcc	961
Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala	Ala	Tyr	Gly	Lys	Ala	
305					310					315					320	
tta	gat	tta	agc	ctc	aac	agt	att	ttc	tt							990
Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe								
				325												

<210> 16
 <211> 329
 <212> PRT
 <213> Unknown

<400> 16
 Asn Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys
 1 5 10 15
 Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe
 20 25 30
 Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu
 35 40 45
 Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu
 50 55 60
 Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu

65					70					75				80	
Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Phe
				85					90					95	
Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys	Asp	Gly	Gly	Ala	Ser	Ile	Asn
			100					105					110		
Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn	Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn
		115					120					125			
Leu	Ser	Ser	Thr	Ser	Leu	Arg	Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn
	130					135					140				
Met	Pro	His	Leu	Lys	Val	Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly
145					150					155					160
Glu	Ile	Ala	Ser	Gly	Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile
				165					170					175	
Leu	Asp	Leu	Ser	Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile
			180					185					190		
Asn	Ile	Ser	Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His
		195					200					205			
Leu	Arg	Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro
	210					215					220				
Leu	Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe
225					230					235					240
Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	Glu
				245					250					255	
Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	Asp	Thr
			260					265					270		
Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	Ile	Arg	Lys
		275					280					285			
Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	Asn	Phe	Tyr	His
	290					295					300				
Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala	Ala	Tyr	Gly	Lys	Ala
305					310					315					320
Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe							
				325											

<210> 17
 <211> 1557

<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (1)..(513)

<220>
<221> misc_feature
<222> (93)..(149)
<223> Xaa translation depends on genetic code

<400> 17
cag tct ctt tcc aca tcc caa act ttc tat gat gct tac att tct tat 48
Gln Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr
1 5 10 15
gac acc aaa gat gcc tct gtt act gac tgg gtg ata aat gag ctg cgc 96
Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg
20 25 30
tac cac ctt gaa gag agc cga gac aaa aac gtt ctc ctt tgt cta gag 144
Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu
35 40 45
gag agg gat tgg gac ccg gga ttg gcc atc atc gac aac ctc atg cag 192
Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln
50 55 60
agc atc aac caa agc aag aaa aca gta ttt gtt tta acc aaa aaa tat 240
Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr
65 70 75 80
gca aaa agc tgg aac ttt aaa aca gct ttt tac ttg gsc ttg cag agg 288
Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Xaa Leu Gln Arg
85 90 95
cta atg ggt gag aac atg gat gtg att ata ttt atc ctg ctg gag cca 336
Leu Met Gly Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro
100 105 110
gtg tta cag cat tct ccg tat ttg agg cta cgg cag cgg atc tgt aag 384
Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys
115 120 125
agc tcc atc ctc cag tgg cct gac aac ccg aag gca gaa agg ttg ttt 432
Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe
130 135 140
tgg caa act ctg wga aat gtg gtc ttg act gaa aat gat tca cgg tat 480

Trp Gln Thr Leu Xaa Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr
 145 150 155 160

aac aat atg tat gtc gat tcc att aag caa tac taactgacgt taagtcatga 533
 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
 165 170

tttcgcgccca taataaagat gcaaaggaat gacatttcng tattagttat ctattgctan 593
 ggtaacnaaa ttantcccaa aaancttang tnggtttnaa aacaacnaca ttntgctggn 653
 cccacagttt ttgaggggtca ggagtccagg cccagcataa ctgggtcttc tgcttcaggg 713
 tgtctncaga ggctgcaatg taggtgttca ccagagacat aggcatcact ggggtcacac 773
 tncatgtggt tgttttctgg attcaattcc tcctgggcta ttggccaaag gctataactca 833
 tgtaagccat gcgagcctat cccacaangg cagcttgctt catcagagct agcaaaaaag 893
 agaggttgct agcaagatga agtcacaatc ttttgtaatc gaatcaaaaa agtgatatct 953
 catcactttg gccatattct atttgttaga agtaaaccac aggtcccacc agctccatgg 1013
 gagtgaccac ctacgtccag ggaaaacagc tgaagaccaa gatgggtgagc tctgattgct 1073
 tcagttgggtc atcaactatt ttcccttgac tgctgtcctg ggatggccgg ctatcttgat 1133
 ggatagattg tgaatatcag gaggccaggg atcactgtgg accatcttag cagttgacct 1193
 aacacatctt cttttcaata tctaagaact tttgccactg tgactaatgg tcctaataatt 1253
 aagctgttgt ttatatattat catatatcta tggtacatg gttatattat gctgtggttg 1313
 ggttcggttt tatttacagt tgcttttaca aatatttgct gtaacatttg acttctaagg 1373
 tttagatgcc atttaagaac tgagatggat agcttttaaa gcatctttta cttcttacca 1433
 ttttttaaaa gtatgcagct aaattcgaag cttttggtct atattgttaa ttgccattgc 1493
 tgtaaactctt aaaatgaatg aataaaaatg tttcatttta aaaaaaaaaa aaaaaaaaaa 1553
 aaaa 1557

<210> 18
 <211> 171
 <212> PRT
 <213> Unknown

<400> 18
 Gln Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr
 1 5 10 15

Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg
 20 25 30
 Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu
 35 40 45
 Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln
 50 55 60
 Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr
 65 70 75 80
 Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Xaa Leu Gln Arg
 85 90 95
 Leu Met Gly Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro
 100 105 110
 Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys
 115 120 125
 Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe
 130 135 140
 Trp Gln Thr Leu Xaa Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr
 145 150 155 160
 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
 165 170

<210> 19
 <211> 629
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (1)..(486)

<220>
 <221> misc_feature
 <222> (48)..(75)
 <223> Xaa translation depends on genetic code

<400> 19
 aat gaa ttg atc ccc aat cta gag aag gaa gat ggt tct atc ttg att 48
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile
 1 5 10 15

tgc ctt tat gaa agc tac ttt gac cct ggc aaa agc att agt gaa aat	96
Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn	
20 25 30	
att gta agc ttc att gag aaa agc tat aag tcc atc ttt gtt ttg tcy	144
Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Xaa	
35 40 45	
ccc aac ttt gtc cag aat gag tgg tgc cat tat gaa ttc tac ttt gcc	192
Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala	
50 55 60	
cac cac aat ctc ttc cat gaa aat tct gat cay ata att ctt atc tta	240
His His Asn Leu Phe His Glu Asn Ser Asp Xaa Ile Ile Leu Ile Leu	
65 70 75 80	
ctg gaa ccc att cca ttc tat tgc att ccc acc agg tat cat aaa ctg	288
Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu	
85 90 95	
gaa gct ctc ctg gaa aaa aaa gca tac ttg gaa tgg ccc aag gat agg	336
Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg	
100 105 110	
cgt aaa tgt ggg ctt ttc tgg gca aac ctt cga gct gct gtt aat gtt	384
Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Val Asn Val	
115 120 125	
aat gta tta gcc acc aga gaa atg tat gaa ctg cag aca ttc aca gag	432
Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu	
130 135 140	
tta aat gaa gag tct cga ggt tct aca atc tct ctg atg aga aca gac	480
Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp	
145 150 155 160	
tgt cta taaaatccca cagtccttgg gaagttgggg accacataca ctggttgggat	536
Cys Leu	
gtacattgat acaaccttta tgatggcaat ttgacaatat ttattaaaat aaaaaatggt	596
tattcccttc aaaaaaaaaa aaaaaaaaaa aaa	629

<210> 20
 <211> 162
 <212> PRT
 <213> Unknown

<400> 20
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile
 1 5 10 15

Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn
 20 25 30
 Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Xaa
 35 40 45
 Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala
 50 55 60
 His His Asn Leu Phe His Glu Asn Ser Asp Xaa Ile Ile Leu Ile Leu
 65 70 75 80
 Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu
 85 90 95
 Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg
 100 105 110
 Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Val Asn Val
 115 120 125
 Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu
 130 135 140
 Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp
 145 150 155 160
 Cys Leu

<210> 21

<211> 427

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (1)..(426)

<400> 21

aag aac tcc aaa gaa aac ctc cag ttt cat gct ttt att tca tat agt 48
 Lys Asn Ser Lys Glu Asn Leu Gln Phe His Ala Phe Ile Ser Tyr Ser
 1 5 10 15

gaa cat gat tct gcc tgg gtg aaa agt gaa ttg gta cct tac cta gaa 96
 Glu His Asp Ser Ala Trp Val Lys Ser Glu Leu Val Pro Tyr Leu Glu
 20 25 30

aaa gaa gat ata cag att tgt ctt cat gag aga aac ttt gtc cct ggc 144

Lys	Glu	Asp	Ile	Gln	Ile	Cys	Leu	His	Glu	Arg	Asn	Phe	Val	Pro	Gly	
		35					40					45				
aag	agc	att	gtg	gaa	aat	atc	atc	aac	tgc	att	gag	aag	agt	tac	aag	192
Lys	Ser	Ile	Val	Glu	Asn	Ile	Ile	Asn	Cys	Ile	Glu	Lys	Ser	Tyr	Lys	
	50					55					60					
tcc	atc	ttt	gtt	ttg	tct	ccc	aac	ttt	gtc	cag	agt	gag	tgg	tgc	cat	240
Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Ser	Glu	Trp	Cys	His	
65					70				75						80	
tac	gaa	ctc	tat	ttt	gcc	cat	cac	aat	ctc	ttt	cat	gaa	gga	tct	aat	288
Tyr	Glu	Leu	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn	
				85					90					95		
aac	tta	atc	ctc	atc	tta	ctg	gaa	ccc	att	cca	cag	aac	agc	att	ccc	336
Asn	Leu	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile	Pro	
			100					105					110			
aac	aag	tac	cac	aag	ctg	aag	gct	ctc	atg	acg	cag	cgg	act	tat	ttg	384
Asn	Lys	Tyr	His	Lys	Leu	Lys	Ala	Leu	Met	Thr	Gln	Arg	Thr	Tyr	Leu	
		115					120					125				
cag	tgg	ccc	aag	gag	aaa	agc	aaa	cgt	ggg	ctc	ttt	tgg	gct	a		427
Gln	Trp	Pro	Lys	Glu	Lys	Ser	Lys	Arg	Gly	Leu	Phe	Trp	Ala			
	130					135					140					
<210>	22															
<211>	142															
<212>	PRT															
<213>	Unknown															
<400>	22															
Lys	Asn	Ser	Lys	Glu	Asn	Leu	Gln	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	
1				5					10					15		
Glu	His	Asp	Ser	Ala	Trp	Val	Lys	Ser	Glu	Leu	Val	Pro	Tyr	Leu	Glu	
		20						25					30			
Lys	Glu	Asp	Ile	Gln	Ile	Cys	Leu	His	Glu	Arg	Asn	Phe	Val	Pro	Gly	
		35					40					45				
Lys	Ser	Ile	Val	Glu	Asn	Ile	Ile	Asn	Cys	Ile	Glu	Lys	Ser	Tyr	Lys	
	50					55					60					
Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Ser	Glu	Trp	Cys	His	
65					70					75					80	
Tyr	Glu	Leu	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn	
				85					90					95		
Asn	Leu	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile	Pro	

100	105	110
Asn Lys Tyr His Lys Leu Lys Ala Leu Met Thr Gln Arg Thr Tyr Leu		
115	120	125
Gln Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe Trp Ala		
130	135	140

<210> 23
 <211> 662
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (1)..(627)
 <220>
 <221> misc_feature
 <222> (18)..(136)
 <223> Xaa translation depends on genetic code

<400> 23	
gct tcc acc tgt gcc tgg cct ggc ttc cct ggc ggg ggc ggc aaa gtg	48
Ala Ser Thr Cys Ala Trp Pro Gly Phe Pro Gly Gly Gly Lys Val	
5 10 15	
ggc gar atg agg atg ccc tgc cct acg atg cct tcg tgg tct tcg aca	96
Gly Xaa Met Arg Met Pro Cys Pro Thr Met Pro Ser Trp Ser Ser Thr	
20 25 30	
aaa cgc rga gcg cag tgg cag act ggg tgt aca acg agc ttc ggg ggc	144
Lys Arg Xaa Ala Gln Trp Gln Thr Gly Cys Thr Thr Ser Phe Gly Gly	
35 40 45	
agc tgg agg agt gcc gtg ggc gct ggg cac tcc gcc tgt gcc tgg agg	192
Ser Trp Arg Ser Ala Val Gly Ala Gly His Ser Ala Cys Ala Trp Arg	
50 55 60	
aac gcg act ggc tgc ctg gca aaa ccc tct ttg aga acc tgt ggg cct	240
Asn Ala Thr Gly Cys Leu Ala Lys Pro Ser Leu Arg Thr Cys Gly Pro	
65 70 75 80	
cgg tct atg gca gcc gca aga cgc tgt ttg tgc tgg ccc aca cgg acc	288
Arg Ser Met Ala Ala Ala Arg Arg Cys Leu Cys Trp Pro Thr Arg Thr	
85 90 95	
ggg tca gtg gtc tct tgc gcg cca ktt ntc ctg ctg gcc cag cag cgc	336
Gly Ser Val Val Ser Cys Ala Pro Xaa Xaa Leu Leu Ala Gln Gln Arg	

100										105					110					
ctg	ctg	gar	gac	cgc	aag	gac	gtc	gtg	gtg	ctg	gtg	atc	cta	ang	cct	384				
Leu	Leu	Xaa	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	Ile	Leu	Xaa	Pro					
		115					120					125								
gac	ggc	caa	gcc	tcc	cga	cta	cnn	gat	gcg	ctg	acc	agc	gcc	tct	gcc	432				
Asp	Gly	Gln	Ala	Ser	Arg	Leu	Xaa	Asp	Ala	Leu	Thr	Ser	Ala	Ser	Ala					
	130					135					140									
gcc	aga	gtg	tcc	tcc	tct	ggc	ccc	acc	agc	cca	gtg	gtc	gcg	cag	ctt	480				
Ala	Arg	Val	Ser	Ser	Ser	Gly	Pro	Thr	Ser	Pro	Val	Val	Ala	Gln	Leu					
145					150					155					160					
ctg	agg	cca	gca	tgc	atg	gcc	ctg	acc	agg	gac	aac	cac	cac	ttc	tat	528				
Leu	Arg	Pro	Ala	Cys	Met	Ala	Leu	Thr	Arg	Asp	Asn	His	His	Phe	Tyr					
				165					170					175						
aac	cgg	aac	ttc	tgc	cag	gga	acc	cac	ggc	cga	ata	gcc	gtg	agc	cgg	576				
Asn	Arg	Asn	Phe	Cys	Gln	Gly	Thr	His	Gly	Arg	Ile	Ala	Val	Ser	Arg					
			180					185					190							
aat	cct	gca	cgg	tgc	cac	ctc	cac	aca	cac	cta	aca	tat	gcc	tgc	ctg	624				
Asn	Pro	Ala	Arg	Cys	His	Leu	His	Thr	His	Leu	Thr	Tyr	Ala	Cys	Leu					
		195				200						205								
atc	tgaccaacac	atgctcgcca	ccctcaccac	acacc												662				
Ile																				

<210> 24

<211> 209

<212> PRT

<213> Unknown

<400> 24

Ala	Ser	Thr	Cys	Ala	Trp	Pro	Gly	Phe	Pro	Gly	Gly	Gly	Gly	Lys	Val
1				5					10					15	

Gly	Xaa	Met	Arg	Met	Pro	Cys	Pro	Thr	Met	Pro	Ser	Trp	Ser	Ser	Thr
			20					25					30		

Lys	Arg	Xaa	Ala	Gln	Trp	Gln	Thr	Gly	Cys	Thr	Thr	Ser	Phe	Gly	Gly
		35				40						45			

Ser	Trp	Arg	Ser	Ala	Val	Gly	Ala	Gly	His	Ser	Ala	Cys	Ala	Trp	Arg
50						55					60				

Asn	Ala	Thr	Gly	Cys	Leu	Ala	Lys	Pro	Ser	Leu	Arg	Thr	Cys	Gly	Pro
65					70					75					80

Arg	Ser	Met	Ala	Ala	Ala	Arg	Arg	Cys	Leu	Cys	Trp	Pro	Thr	Arg	Thr
				85					90					95	

Gly	Ser	Val	Val	Ser	Cys	Ala	Pro	Xaa	Xaa	Leu	Leu	Ala	Gln	Gln	Arg	
			100					105					110			
Leu	Leu	Xaa	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	Ile	Leu	Xaa	Pro	
		115					120					125				
Asp	Gly	Gln	Ala	Ser	Arg	Leu	Xaa	Asp	Ala	Leu	Thr	Ser	Ala	Ser	Ala	
	130					135					140					
Ala	Arg	Val	Ser	Ser	Ser	Gly	Pro	Thr	Ser	Pro	Val	Val	Ala	Gln	Leu	
145					150					155					160	
Leu	Arg	Pro	Ala	Cys	Met	Ala	Leu	Thr	Arg	Asp	Asn	His	His	Phe	Tyr	
				165					170					175		
Asn	Arg	Asn	Phe	Cys	Gln	Gly	Thr	His	Gly	Arg	Ile	Ala	Val	Ser	Arg	
		180						185					190			
Asn	Pro	Ala	Arg	Cys	His	Leu	His	Thr	His	Leu	Thr	Tyr	Ala	Cys	Leu	
	195					200						205				

Ile

<210> 25
 <211> 4865
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (107)..(2617)

<220>
 <221> mat_peptide
 <222> (173)..(2617)

<220>
 <221> misc_feature
 <222> (189)
 <223> Xaa translation depends on genetic code

<400> 25
 aaaataactcc cttgcctcaa aaactgctcg gtcaaacggt gatagcaaac cacgcattca 60
 cagggccact gctgctcaca naascagtga ggatgatgcc aggatg atg tct gcc 115
 Met Ser Ala
 -20

tcg	cgc	ctg	gct	ggg	act	ctg	atc	cca	gcc	atg	gcc	ttc	ctc	tcc	tgc	163
Ser	Arg	Leu	Ala	Gly	Thr	Leu	Ile	Pro	Ala	Met	Ala	Phe	Leu	Ser	Cys	
				-15					-10					-5		
gtg	aga	cca	gaa	agc	tgg	gag	ccc	tgc	gtg	gag	ggt	cct	aat	att	act	211
Val	Arg	Pro	Glu	Ser	Trp	Glu	Pro	Cys	Val	Glu	Val	Pro	Asn	Ile	Thr	
		-1	1				5					10				
tat	caa	tgc	atg	gag	ctg	aat	ttc	tac	aaa	atc	ccc	gac	aac	ctc	ccc	259
Tyr	Gln	Cys	Met	Glu	Leu	Asn	Phe	Tyr	Lys	Ile	Pro	Asp	Asn	Leu	Pro	
	15					20					25					
ttc	tca	acc	aag	aac	ctg	gac	ctg	agc	ttt	aat	ccc	ctg	agg	cat	tta	307
Phe	Ser	Thr	Lys	Asn	Leu	Asp	Leu	Ser	Phe	Asn	Pro	Leu	Arg	His	Leu	
	30				35					40					45	
ggc	agc	tat	agc	ttc	ttc	agt	ttc	cca	gaa	ctg	cag	gtg	ctg	gat	tta	355
Gly	Ser	Tyr	Ser	Phe	Phe	Ser	Phe	Pro	Glu	Leu	Gln	Val	Leu	Asp	Leu	
				50					55					60		
tcc	agg	tgt	gaa	atc	cag	aca	att	gaa	gat	ggg	gca	tat	cag	agc	cta	403
Ser	Arg	Cys	Glu	Ile	Gln	Thr	Ile	Glu	Asp	Gly	Ala	Tyr	Gln	Ser	Leu	
			65					70					75			
agc	cac	ctc	tct	acc	tta	ata	ttg	aca	gga	aac	ccc	atc	cag	agt	tta	451
Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Thr	Gly	Asn	Pro	Ile	Gln	Ser	Leu	
		80					85					90				
gcc	ctg	gga	gcc	ttt	tct	gga	cta	tca	agt	tta	cag	aag	ctg	gtg	gct	499
Ala	Leu	Gly	Ala	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Lys	Leu	Val	Ala	
	95					100					105					
gtg	gag	aca	aat	cta	gca	tct	cta	gag	aac	ttc	ccc	att	gga	cat	ctc	547
Val	Glu	Thr	Asn	Leu	Ala	Ser	Leu	Glu	Asn	Phe	Pro	Ile	Gly	His	Leu	
	110				115					120					125	
aaa	act	ttg	aaa	gaa	ctt	aat	gtg	gct	cac	aat	ctt	atc	caa	tct	ttc	595
Lys	Thr	Leu	Lys	Glu	Leu	Asn	Val	Ala	His	Asn	Leu	Ile	Gln	Ser	Phe	
				130					135					140		
aaa	tta	cct	gag	tat	ttt	tct	aat	ctg	acc	aat	cta	gag	cac	ttg	gac	643
Lys	Leu	Pro	Glu	Tyr	Phe	Ser	Asn	Leu	Thr	Asn	Leu	Glu	His	Leu	Asp	
			145					150					155			
ctt	tcc	agc	aac	aag	att	caa	agt	att	tat	tgc	aca	gac	ttg	cgg	gtt	691
Leu	Ser	Ser	Asn	Lys	Ile	Gln	Ser	Ile	Tyr	Cys	Thr	Asp	Leu	Arg	Val	
		160					165					170				
cta	cat	caa	atg	ccc	cta	ctc	aat	ctc	tct	tta	gac	ctg	tcc	ctg	aay	739
Leu	His	Gln	Met	Pro	Leu	Leu	Asn	Leu	Ser	Leu	Asp	Leu	Ser	Leu	Xaa	
	175					180					185					

cct Pro 190	atg Met	aac Asn	ttt Phe	atc Ile	caa Gln 195	cca Pro	ggc Gly	gca Ala	ttt Phe	aaa Lys 200	gaa Glu	att Ile	agg Arg	ctt Leu	cat His 205	787
aag Lys	ctg Leu	act Thr	tta Leu	aga Arg 210	aat Asn	aat Asn	ttt Phe	gat Asp	agt Ser 215	tta Leu	aat Asn	gta Val	atg Met	aaa Lys 220	act Thr	835
tgt Cys	att Ile	caa Gln 225	ggc Gly 225	ctg Leu	gct Ala	ggc Gly	tta Leu	gaa Glu 230	gtc Val	cat His	cgt Arg	ttg Leu	gtt Val 235	ctg Leu	gga Gly	883
gaa Glu	ttt Phe	aga Arg 240	aat Asn	gaa Glu	gga Gly	aac Asn	ttg Leu 245	gaa Glu	aag Lys	ttt Phe	gac Asp	aaa Lys 250	tct Ser	gct Ala	cta Leu	931
gag Glu	ggc Gly 255	ctg Leu	tgc Cys	aat Asn	ttg Leu 260	acc Thr	att Ile	gaa Glu	gaa Glu	ttc Phe	cga Arg 265	tta Leu	gca Ala	tac Tyr	tta Leu	979
gac Asp 270	tac Tyr	tac Tyr	ctc Leu	gat Asp	gat Asp 275	att Ile	att Ile	gac Asp	tta Leu	ttt Phe 280	aat Asn	tgt Cys	ttg Leu	aca Thr	aat Asn 285	1027
gtt Val	tct Ser	tca Ser	ttt Phe	tcc Ser 290	ctg Leu	gtg Val	agt Ser	gtg Val	act Thr 295	att Ile	gaa Glu	agg Arg	gta Val	aaa Lys 300	gac Asp	1075
ttt Phe	tct Ser	tat Tyr	aat Asn 305	ttc Phe	gga Gly	tgg Trp	caa Gln	cat His 310	tta Leu	gaa Glu	tta Leu	gtt Val	aac Asn 315	tgt Cys	aaa Lys	1123
ttt Phe	gga Gly 320	cag Gln	ttt Phe	ccc Pro	aca Thr	ttg Leu	aaa Lys 325	ctc Leu	aaa Lys	tct Ser	ctc Leu	aaa Lys 330	agg Arg	ctt Leu	act Thr	1171
ttc Phe 335	act Thr	tcc Ser	aac Asn	aaa Lys	ggc Gly 340	ggg Gly	aat Asn	gct Ala	ttt Phe	tca Ser	gaa Glu 345	gtt Val	gat Asp	cta Leu	cca Pro	1219
agc Ser 350	ctt Leu	gag Glu	ttt Phe	cta Leu	gat Asp 355	ctc Leu	agt Ser	aga Arg	aat Asn	ggc Gly 360	ttg Leu	agt Ser	ttc Phe	aaa Lys	ggc Gly 365	1267
tgc Cys	tgt Cys	tct Ser	caa Gln	agt Ser 370	gat Asp	ttt Phe	ggg Gly	aca Thr	acc Thr 375	agc Ser	cta Leu	aag Lys	tat Tyr	tta Leu 380	gat Asp	1315
ctg Leu	agc Ser	ttc Phe	aat Asn 385	ggc Gly	gtt Val	att Ile	acc Thr	atg Met 390	agt Ser	tca Ser	aac Asn	ttc Phe	ttg Leu 395	ggc Gly	tta Leu	1363
gaa Glu	caa Gln	cta Leu	gaa Glu	cat His	ctg Leu	gat Asp	ttc Phe	cag Gln	cat His	tcc Ser	aat Asn	ttg Leu	aaa Lys	caa Gln	atg Met	1411

400					405					410						
agt	gag	ttt	tca	gta	ttc	cta	tca	ctc	aga	aac	ctc	att	tac	ctt	gac	1459
Ser	Glu	Phe	Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp	
	415					420					425					
att	tct	cat	act	cac	acc	aga	gtt	gct	ttc	aat	ggc	atc	ttc	aat	ggc	1507
Ile	Ser	His	Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly	
430					435					440					445	
ttg	tcc	agt	ctc	gaa	gtc	ttg	aaa	atg	gct	ggc	aat	tct	ttc	cag	gaa	1555
Leu	Ser	Ser	Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Glu	
				450					455					460		
aac	ttc	ctt	cca	gat	atc	ttc	aca	gag	ctg	aga	aac	ttg	acc	ttc	ctg	1603
Asn	Phe	Leu	Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu	
			465					470					475			
gac	ctc	tct	cag	tgt	caa	ctg	gag	cag	ttg	tct	cca	aca	gca	ttt	aac	1651
Asp	Leu	Ser	Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn	
		480					485					490				
tca	ctc	tcc	agt	ctt	cag	gta	cta	aat	atg	agc	cac	aac	aac	ttc	ttt	1699
Ser	Leu	Ser	Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe	
	495					500					505					
tca	ttg	gat	acg	ttt	cct	tat	aag	tgt	ctg	aac	tcc	ctc	cag	gtt	ctt	1747
Ser	Leu	Asp	Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu	
510					515					520					525	
gat	tac	agt	ctc	aat	cac	ata	atg	act	tcc	aaa	aaa	cag	gaa	cta	cag	1795
Asp	Tyr	Ser	Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln	
				530					535					540		
cat	ttt	cca	agt	agt	cta	gct	ttc	tta	aat	ctt	act	cag	aat	gac	ttt	1843
His	Phe	Pro	Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe	
			545					550					555			
gct	tgt	act	tgt	gaa	cac	cag	agt	ttc	ctg	caa	tgg	atc	aag	gac	cag	1891
Ala	Cys	Thr	Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln	
		560					565					570				
agg	cag	ctc	ttg	gtg	gaa	gtt	gaa	cga	atg	gaa	tgt	gca	aca	cct	tca	1939
Arg	Gln	Leu	Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser	
	575					580					585					
gat	aag	cag	ggc	atg	cct	gtg	ctg	agt	ttg	aat	atc	acc	tgt	cag	atg	1987
Asp	Lys	Gln	Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met	
590					595					600					605	
aat	aag	acc	atc	att	ggc	gtg	tcg	gtc	ctc	agt	gtg	ctt	gta	gta	tct	2035
Asn	Lys	Thr	Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser	
				610					615					620		

gtt gta gca gtt ctg gtc tat aag ttc tat ttt cac ctg atg ctt ctt	2083
Val Val Ala Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu	
625 630 635	
gct ggc tgc ata aag tat ggt aga ggt gaa aac atc tat gat gcc ttt	2131
Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe	
640 645 650	
gtt atc tac tca agc cag gat gag gac tgg gta agg aat gag cta gta	2179
Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val	
655 660 665	
aag aat tta gaa gaa ggg gtg cct cca ttt cag ctc tgc ctt cac tac	2227
Lys Asn Leu Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr	
670 675 680 685	
aga gac ttt att ccc ggt gtg gcc att gct gcc aac atc atc cat gaa	2275
Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu	
690 695 700	
ggg ttc cat aaa agc cga aag gtg att gtt gtg gtg tcc cag cac ttc	2323
Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe	
705 710 715	
atc cag agc cgc tgg tgt atc ttt gaa tat gag att gct cag acc tgg	2371
Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp	
720 725 730	
cag ttt ctg agc agt cgt gct ggt atc atc ttc att gtc ctg cag aag	2419
Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys	
735 740 745	
gtg gag aag acc ctg ctc agg cag cag gtg gag ctg tac cgc ctt ctc	2467
Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu	
750 755 760 765	
agc agg aac act tac ctg gag tgg gag gac agt gtc ctg ggg cgg cac	2515
Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His	
770 775 780	
atc ttc tgg aga cga ctc aga aaa gcc ctg ctg gat ggt aaa tca tgg	2563
Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp	
785 790 795	
aat cca gaa gga aca gtg ggt aca gga tgc aat tgg cag gaa gca aca	2611
Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr	
800 805 810	
tct atc tgaagaggaa aaataaaaac ctccctgaggc atttcttgcc cagctgggctc	2667
Ser Ile	
815	
caacacttgt tcagttaata agtattaaat gctgccacat gtcaggcctt atgctaaggg	2727

tgagtaattc catggtgcac tagatatgca gggctgctaa tctcaaggag cttccagtgc 2787
 agagggaata aatgctagac taaaatacag agtcttccag gtgggcattt caaccaactc 2847
 agtcaaggaa cccatgacaa agaaagtcac ttcaactctt acctcatcaa gttgaataaa 2907
 gacagagaaa acagaaagag acattgttct tttcctgagt cttttgaatg gaaattgtat 2967
 tatgttatag ccatcataaa accatttttg tagttttgac tgaactgggt gttcactttt 3027
 tcctttttga ttgaatacaa tttaaattct acttgatgac tgcagtcgtc aaggggctcc 3087
 tgatgcaaga tgccccttcc attttaagtc tgtctcctta cagakgttaa agtctantgg 3147
 ctaattccta aggaaacctg attaacacat gtcacaacc atcctgggtca ttctcgancc 3207
 tgttctatct ttttaactaat caccctgat atatttttat ttttatatat ccagttttca 3267
 tttttttacg tcttgccctat aagctaatat cataaataag gttgttttaag acgtgcttca 3327
 aatattccata ttaaccacta tttttcaagg aagtatggaa aagtacactc tgtcactttg 3387
 tcaactgatg tcattccaaa gttattgcct actaagtaat gactgtcatg aaagcagcat 3447
 tgaataaatt tgtttaaagg gggcactctt ttaaaccgga agaaaatttc cgcttcctgg 3507
 ttttatcatg gacaatttgg gctakaggca kgaaggaggt gggatkacct caggangtca 3567
 ccttttcttg attccagaaa catatgggct gataaaccgc gggtgacctc atgaaatgag 3627
 ttgcagcaga wgtttatctt tttcagaaca agtgatgttt gatggacctm tgaatctmtt 3687
 tagggagaca cagatggctg ggatccctcc cctgtacctt tctcactgmc aggagaacta 3747
 cgtgtgaagg tattcaaggc agggagtata cattgctggt tcctgttggg caatgctcct 3807
 tgaccacatt ttgggaagag tggatgttat cattgagaaa acaatgtgtc tggaaattaat 3867
 ggggttctta taaagaaggc tcccagaaaa gaatgttcat tccagcttct tcaggaaaca 3927
 ggaacattca aggaaaagga caatcaggat gtcacacagg aatgaaaaat aaaaaccaca 3987
 atgagatatc acctataacc aggtagatgg ctactataaa aaaatgaagt gtcacacagg 4047
 atatagagaa attggaacct ttcttcactg ctggagggaa tggaaaatgg tgtagccgtt 4107
 atgaaaaaca gtacggaggc ttctcaaaaa ttaaaaatag aactgctata tgatccagca 4167
 atctcacttc tgtatatata cccaaaataa ttgaaatcag aatttcaaga aatatattac 4227
 actcccatgt tcattgtggc actcttcaca atcactgttt ccaaagttat ggaaacaacc 4287

caaattttcca ttggaaaata aatggacaaa ggaaatgtgc atataacgta caatggggat 4347
 attattcagc ctaaaaaaag gggggatcct gttatztatg acaacatgaa taaacccgga 4407
 ggccattatg ctatgtaaaa tgagcaagta acagaaagac aaatactgcc tgatttcatt 4467
 tatatgaggt tctaaaatag tcaaactcat agaagcagag aatagaacag tggttcctag 4527
 ggaaaaggag gaagggagaa atgaggaaat agggagttgt ctaattggta taaaattata 4587
 gtatgcaaga tgaattagct ctaaagatca gctgtatagc agagttcgta taatgaacaa 4647
 tactgtatta tgcacttaac attttggtta gagggtagct ctcatgttaa gtgttcttac 4707
 catatacata tacacaagga agcttttgga ggtgatggat atatttatta ccttgattgt 4767
 ggtgatgggt tgacaggtat gtgactatgt ctaaactcat caaattgtat acattaaata 4827
 tatgcagttt tataatatca aaaaaaaaaa aaaaaaaaaa 4865

<210> 26
 <211> 837
 <212> PRT
 <213> Unknown

<400> 26

Met	Ser	Ala	Ser	Arg	Leu	Ala	Gly	Thr	Leu	Ile	Pro	Ala	Met	Ala	Phe
		-20					-15					-10			
Leu	Ser	Cys	Val	Arg	Pro	Glu	Ser	Trp	Glu	Pro	Cys	Val	Glu	Val	Pro
	-5				-1	1				5					10
Asn	Ile	Thr	Tyr	Gln	Cys	Met	Glu	Leu	Asn	Phe	Tyr	Lys	Ile	Pro	Asp
				15					20					25	
Asn	Leu	Pro	Phe	Ser	Thr	Lys	Asn	Leu	Asp	Leu	Ser	Phe	Asn	Pro	Leu
			30					35					40		
Arg	His	Leu	Gly	Ser	Tyr	Ser	Phe	Phe	Ser	Phe	Pro	Glu	Leu	Gln	Val
		45					50					55			
Leu	Asp	Leu	Ser	Arg	Cys	Glu	Ile	Gln	Thr	Ile	Glu	Asp	Gly	Ala	Tyr
	60					65					70				
Gln	Ser	Leu	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Thr	Gly	Asn	Pro	Ile
	75				80					85					90
Gln	Ser	Leu	Ala	Leu	Gly	Ala	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Lys
				95					100					105	
Leu	Val	Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Leu	Glu	Asn	Phe	Pro	Ile
			110				115						120		

Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn Leu Ile
 125 130 135
 Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu
 140 145 150
 His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp
 155 160 165 170
 Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu
 175 180 185
 Ser Leu Xaa Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile
 190 195 200
 Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val
 205 210 215
 Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu
 220 225 230
 Val Leu Gly Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys
 235 240 245 250
 Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu
 255 260 265
 Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys
 270 275 280
 Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg
 285 290 295
 Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val
 300 305 310
 Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys
 315 320 325 330
 Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser Glu Val
 335 340 345
 Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser
 350 355 360
 Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys
 365 370 375
 Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe
 380 385 390
 Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu
 395 400 405 410

Lys	Gln	Met	Ser	Glu	Phe	Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	415	420	425
Tyr	Leu	Asp	Ile	Ser	His	Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	430	435	440
Phe	Asn	Gly	Leu	Ser	Ser	Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	445	450	455
Phe	Gln	Glu	Asn	Phe	Leu	Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	460	465	470
Thr	Phe	Leu	Asp	Leu	Ser	Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	475	480	485
Ala	Phe	Asn	Ser	Leu	Ser	Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	495	500	505
Asn	Phe	Phe	Ser	Leu	Asp	Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	510	515	520
Gln	Val	Leu	Asp	Tyr	Ser	Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	525	530	535
Glu	Leu	Gln	His	Phe	Pro	Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	540	545	550
Asn	Asp	Phe	Ala	Cys	Thr	Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	555	560	565
Lys	Asp	Gln	Arg	Gln	Leu	Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	575	580	585
Thr	Pro	Ser	Asp	Lys	Gln	Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	590	595	600
Cys	Gln	Met	Asn	Lys	Thr	Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	605	610	615
Val	Val	Ser	Val	Val	Ala	Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu	620	625	630
Met	Leu	Leu	Ala	Gly	Cys	Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	Ile	Tyr	635	640	645
Asp	Ala	Phe	Val	Ile	Tyr	Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn	655	660	665
Glu	Leu	Val	Lys	Asn	Leu	Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys	670	675	680
Leu	His	Tyr	Arg	Asp	Phe	Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile	685	690	695

Ile	His	Glu	Gly	Phe	His	Lys	Ser	Arg	Lys	Val	Ile	Val	Val	Val	Ser
700						705					710				
Gln	His	Phe	Ile	Gln	Ser	Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	Ile	Ala
715					720					725					730
Gln	Thr	Trp	Gln	Phe	Leu	Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	Ile	Val
				735					740					745	
Leu	Gln	Lys	Val	Glu	Lys	Thr	Leu	Leu	Arg	Gln	Gln	Val	Glu	Leu	Tyr
			750					755					760		
Arg	Leu	Leu	Ser	Arg	Asn	Thr	Tyr	Leu	Glu	Trp	Glu	Asp	Ser	Val	Leu
	765						770					775			
Gly	Arg	His	Ile	Phe	Trp	Arg	Arg	Leu	Arg	Lys	Ala	Leu	Leu	Asp	Gly
780						785					790				
Lys	Ser	Trp	Asn	Pro	Glu	Gly	Thr	Val	Gly	Thr	Gly	Cys	Asn	Trp	Gln
795					800					805					810
Glu	Ala	Thr	Ser	Ile											
				815											

<210> 27

<211> 300

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>

<221> CDS

<222> (1)..(300)

<220>

<221> misc_feature

<222> (62)..(100)

<223> Xaa translation depends on genetic code

<400> 27

tcc	tat	tct	atg	gaa	aaa	gat	gct	ttc	cta	ttt	atg	aga	aat	ttg	aag	48
Ser	Tyr	Ser	Met	Glu	Lys	Asp	Ala	Phe	Leu	Phe	Met	Arg	Asn	Leu	Lys	
1				5				10						15		

gtt	ctc	tca	cta	aaa	gat	aac	aat	gtc	aca	gct	gtc	ccc	acc	act	ttg	96
Val	Leu	Ser	Leu	Lys	Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Thr	Leu	
			20					25					30			

cca cct aat tta cta gag ctc tat ctt tat aac aat atc att aag aaa	144
Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
35 40 45	
atc caa gaa aat gat ttc aat aac ctc aat gag ttg caa gtn ctt gac	192
Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Xaa Leu Asp	
50 55 60	
cta ngt gga aat tgc cct cga tgt nat aat gtc cca tat ccg tgt aca	240
Leu Xaa Gly Asn Cys Pro Arg Cys Xaa Asn Val Pro Tyr Pro Cys Thr	
65 70 75 80	
ccg tgt gaa aat aat tcc ccc tta cag atc cat gan aat gct ttc aat	288
Pro Cys Glu Asn Asn Ser Pro Leu Gln Ile His Xaa Asn Ala Phe Asn	
85 90 95	
tca tcg aca gan	300
Ser Ser Thr Xaa	
100	

<210> 28
 <211> 100
 <212> PRT
 <213> Unknown

<400> 28	
Ser Tyr Ser Met Glu Lys Asp Ala Phe Leu Phe Met Arg Asn Leu Lys	
1 5 10 15	
Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu	
20 25 30	
Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
35 40 45	
Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Xaa Leu Asp	
50 55 60	
Leu Xaa Gly Asn Cys Pro Arg Cys Xaa Asn Val Pro Tyr Pro Cys Thr	
65 70 75 80	
Pro Cys Glu Asn Asn Ser Pro Leu Gln Ile His Xaa Asn Ala Phe Asn	
85 90 95	
Ser Ser Thr Xaa	
100	

<210> 29
 <211> 1756
 <212> DNA
 <213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>

<221> CDS

<222> (1)..(1182)

<400> 29

tct	cca	gaa	att	ccc	tgg	aat	tcc	ttg	cct	cct	gag	gtt	ttt	gag	ggg	48
Ser	Pro	Glu	Ile	Pro	Trp	Asn	Ser	Leu	Pro	Pro	Glu	Val	Phe	Glu	Gly	
1				5				10					15			
atg	ccg	cca	aat	cta	aag	aat	ctc	tcc	ttg	gcc	aaa	aat	ggg	ctc	aaa	96
Met	Pro	Pro	Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	
			20				25						30			
tct	ttc	ttt	tgg	gac	aga	ctc	cag	tta	ctg	aag	cat	ttg	gaa	att	ttg	144
Ser	Phe	Phe	Trp	Asp	Arg	Leu	Gln	Leu	Leu	Lys	His	Leu	Glu	Ile	Leu	
		35					40					45				
gac	ctc	agc	cat	aac	cag	ctg	aca	aaa	gta	cct	gag	aga	ttg	gcc	aac	192
Asp	Leu	Ser	His	Asn	Gln	Leu	Thr	Lys	Val	Pro	Glu	Arg	Leu	Ala	Asn	
	50					55					60					
tgt	tcc	aaa	agt	ctc	aca	aca	ctg	att	ctt	aag	cat	aat	caa	atc	agg	240
Cys	Ser	Lys	Ser	Leu	Thr	Thr	Leu	Ile	Leu	Lys	His	Asn	Gln	Ile	Arg	
65					70				75					80		
caa	ttg	aca	aaa	tat	ttt	cta	gaa	gat	gct	ttg	caa	ttg	cgc	tat	cta	288
Gln	Leu	Thr	Lys	Tyr	Phe	Leu	Glu	Asp	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	
				85				90					95			
gac	atc	agt	tca	aat	aaa	atc	cag	gtc	att	cag	aag	act	agc	ttc	cca	336
Asp	Ile	Ser	Ser	Asn	Lys	Ile	Gln	Val	Ile	Gln	Lys	Thr	Ser	Phe	Pro	
			100					105					110			
gaa	aat	gtc	ctc	aac	aat	ctg	gag	atg	ttg	gtt	tta	cat	cac	aat	cgc	384
Glu	Asn	Val	Leu	Asn	Asn	Leu	Glu	Met	Leu	Val	Leu	His	His	Asn	Arg	
		115					120					125				
ttt	ctt	tgc	aac	tgt	gat	gct	gtg	tgg	ttt	gtc	tgg	tgg	gtt	aac	cat	432
Phe	Leu	Cys	Asn	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His	
	130					135					140					
aca	gat	gtt	act	att	cca	tac	ctg	gcc	act	gat	gtg	act	tgt	gta	ggg	480
Thr	Asp	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly	
145					150				155					160		
cca	gga	gca	cac	aaa	ggg	caa	agt	gtc	ata	tcc	ctt	gat	ctg	tat	acg	528
Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	Thr	
				165				170						175		

tgt	gag	tta	gat	ctc	aca	aac	ctg	att	ctg	ttc	tca	gtt	tcc	ata	tca	576
Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Val	Ser	Ile	Ser	
		180						185					190			
tca	gtc	ctc	ttt	ctt	atg	gta	gtt	atg	aca	aca	agt	cac	ctc	ttt	ttc	624
Ser	Val	Leu	Phe	Leu	Met	Val	Val	Met	Thr	Thr	Ser	His	Leu	Phe	Phe	
		195					200					205				
tgg	gat	atg	tgg	tac	att	tat	tat	ttt	tgg	aaa	gca	aag	ata	aag	ggg	672
Trp	Asp	Met	Trp	Tyr	Ile	Tyr	Tyr	Phe	Trp	Lys	Ala	Lys	Ile	Lys	Gly	
	210					215					220					
tat	cca	gca	tct	gca	atc	cca	tgg	agt	cct	tgt	tat	gat	gct	ttt	att	720
Tyr	Pro	Ala	Ser	Ala	Ile	Pro	Trp	Ser	Pro	Cys	Tyr	Asp	Ala	Phe	Ile	
225					230					235					240	
gtg	tat	gac	act	aaa	aac	tca	gct	gtg	aca	gaa	tgg	gtt	ttg	cag	gag	768
Val	Tyr	Asp	Thr	Lys	Asn	Ser	Ala	Val	Thr	Glu	Trp	Val	Leu	Gln	Glu	
				245					250					255		
ctg	gtg	gca	aaa	ttg	gaa	gat	cca	aga	gaa	aaa	cac	ttc	aat	ttg	tgt	816
Leu	Val	Ala	Lys	Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	
			260					265					270			
cta	gaa	gaa	aga	gac	tgg	cta	cca	gga	cag	cca	gtt	cta	gaa	aac	ctt	864
Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	
		275					280					285				
tct	cag	agc	ata	cag	ctc	agc	aaa	aag	aca	gtg	ttt	gtg	atg	aca	cag	912
Ser	Gln	Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Gln	
	290					295					300					
aaa	tat	gct	aag	act	gag	agt	ttt	aag	atg	gca	ttt	tat	ttg	tct	cat	960
Lys	Tyr	Ala	Lys	Thr	Glu	Ser	Phe	Lys	Met	Ala	Phe	Tyr	Leu	Ser	His	
305					310					315					320	
cag	agg	ctc	ctg	gat	gaa	aaa	gtg	gat	gtg	att	atc	ttg	ata	ttc	ttg	1008
Gln	Arg	Leu	Leu	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	Leu	
				325					330					335		
gaa	aga	cct	ctt	cag	aag	tct	aag	ttt	ctt	cag	ctc	agg	aag	aga	ctc	1056
Glu	Arg	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	Leu	
			340					345					350			
tgc	agg	agc	tct	gtc	ctt	gag	tgg	cct	gca	aat	cca	cag	gct	cac	cca	1104
Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	Pro	
		355					360					365				
tac	ttc	tgg	cag	tgc	ctg	aaa	aat	gcc	ctg	acc	aca	gac	aat	cat	gtg	1152
Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	Val	
	370					375					380					
gct	tat	agt	caa	atg	ttc	aag	gaa	aca	gtc	tagctctctg	aagaatgtca					1202
Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val							

385

390

ccacctagga catgccttgg tacctgaagt tttcataaag gtttccataa atgaaggtct 1262
 gaatttttcc taacagttgt catggctcag attggtggga aatcatcaat atatggctaa 1322
 gaaattaaga aggggagact gatagaagat aatttctttc ttcattgtgcc atgctcagtt 1382
 aaatatttcc cctagctcaa atctgaaaaa ctgtgcctag gagacaacac aaggctttga 1442
 tttatctgca tacaattgat aagagccaca catctgccct gaagaagtac tagtagtttt 1502
 agtagtaggg taaaaattac acaagctttc tctctctctg atactgaact gtaccagagt 1562
 tcaatgaaat aaaagcccag agaacttctc agtaaattgg ttcattatca ttagtagtatcc 1622
 accatgcaat atgccacaaa rccgctactg gtacaggaca gntggtagct gcttcaakgc 1682
 ctcttatcat tttcttgggg cccatggagg ggttctytgg gaaadaggga agkttttttt 1742
 tggccatcca tgaa 1756

<210> 30

<211> 394

<212> PRT

<213> Unknown

<400> 30

Ser Pro Glu Ile Pro Trp Asn Ser Leu Pro Pro Glu Val Phe Glu Gly
 1 5 10 15

Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys
 20 25 30

Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile Leu
 35 40 45

Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala Asn
 50 55 60

Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile Arg
 65 70 75 80

Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr Leu
 85 90 95

Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe Pro
 100 105 110

Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn Arg
 115 120 125

Phe	Leu	Cys	Asn	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His
130						135					140				
Thr	Asp	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly
145					150					155					160
Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	Thr
				165					170					175	
Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Val	Ser	Ile	Ser
			180					185					190		
Ser	Val	Leu	Phe	Leu	Met	Val	Val	Met	Thr	Thr	Ser	His	Leu	Phe	Phe
		195					200					205			
Trp	Asp	Met	Trp	Tyr	Ile	Tyr	Tyr	Phe	Trp	Lys	Ala	Lys	Ile	Lys	Gly
	210					215					220				
Tyr	Pro	Ala	Ser	Ala	Ile	Pro	Trp	Ser	Pro	Cys	Tyr	Asp	Ala	Phe	Ile
225					230					235					240
Val	Tyr	Asp	Thr	Lys	Asn	Ser	Ala	Val	Thr	Glu	Trp	Val	Leu	Gln	Glu
				245					250					255	
Leu	Val	Ala	Lys	Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys
			260					265					270		
Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu
		275					280					285			
Ser	Gln	Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Gln
	290					295					300				
Lys	Tyr	Ala	Lys	Thr	Glu	Ser	Phe	Lys	Met	Ala	Phe	Tyr	Leu	Ser	His
305					310					315					320
Gln	Arg	Leu	Leu	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	Leu
				325					330					335	
Glu	Arg	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	Leu
			340					345					350		
Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	Pro
		355					360					365			
Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	Val
	370					375					380				
Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val						
385					390										

<210> 31
<211> 999

<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (2)..(847)

<220>
<221> misc_feature
<222> (1)..(282)
<223> Xaa translation depends on genetic code

<400> 31
c tcn gat gcc aag att cgg cac nag gca tat tca gag gtc atg atg gtt 49
Xaa Asp Ala Lys Ile Arg His Xaa Ala Tyr Ser Glu Val Met Met Val
1 5 10 15
gga ctgg tca gat tca tac acc tgt gaa tac cct tta aac cta agg gga 97
Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly
20 25 30
act agg tta aaa gac gtt cat ctc cac gaa tta tct tgc aac aca gct 145
Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr Ala
35 40 45
ctg ttg att gtc acc att gtg gtt att atg cta gtt ctg ggg ttg gct 193
Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala
50 55 60
gtg gcc ttc tgc tgt ctc cac ttt gat ctg ccc tgg tat ctc agg atg 241
Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg Met
65 70 75 80
cta ggt caa tgc aca caa aca tgg cac agg gtt agg aaa aca acc caa 289
Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln
85 90 95
gaa caa ctc aag aga aat gtc cga ttc cac gca ttt att tca tac agt 337
Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser
100 105 110
gaa cat gat tct ctg tgg gtg aag aat gaa ttg atc ccc aat cta gag 385
Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu
115 120 125
aag gaa gat ggt tct atc ttg att tgc ctt tat gaa agc tac ttt gac 433
Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp
130 135 140

cct ggc aaa agc att agt gaa aat att gta agc ttc att gag aaa agc	481
Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser	
145 150 155 160	
tat aag tcc atc ttt gtt ttg tct ccc aac ttt gtc cag aat gag tgg	529
Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp	
165 170 175	
tgc cat tat gaa ttc tac ttt gcc cac cac aat ctc ttc cat gaa aat	577
Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu Asn	
180 185 190	
tct gat cac ata att ctt atc tta ctg gaa ccc att cca ttc tat tgc	625
Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr Cys	
195 200 205	
att ccc acc agg tat cat aaa ctg raa gct ctc ctg gaa aaa aaa gca	673
Ile Pro Thr Arg Tyr His Lys Leu Xaa Ala Leu Leu Glu Lys Lys Ala	
210 215 220	
tac ttg gaa tgg ccc aag gat agg cgt aaa tgt ggg ctt tty tgg gca	721
Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Xaa Trp Ala	
225 230 235 240	
aac ctt cga gct gct gtt aat gtt aat gta tta gcc acc aga gaa atg	769
Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu Met	
245 250 255	
tat gaa ctg cag aca ttc aca gag tta aat gaa gag tct cga ggt tct	817
Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser	
260 265 270	
aca atc tyt ctg atg aga aca gac tgt yta taaaatccca cagtccttgg	867
Thr Ile Xaa Leu Met Arg Thr Asp Cys Xaa	
275 280	
gaagttgggg accacataca ctgttgggat gtacattgat acaaccttta tgatggcaat	927
ttgacaatat ttattaaaat aaaaaatggt tattcccttc aaaaaaaaaa aaaaaaaaaa	987
aaaaaaaaaa aa	999

<210> 32
 <211> 282
 <212> PRT
 <213> Unknown

<400> 32
 Xaa Asp Ala Lys Ile Arg His Xaa Ala Tyr Ser Glu Val Met Met Val
 1 5 10 15
 Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly
 20 25 30

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (1)..(1008)

<220>

<221> misc_feature

<222> (285)

<223> Xaa translation depends on genetic code

<400> 33

ctg	cct	gct	ggc	acc	cgg	ctc	cgg	agg	ctg	gat	gtc	agc	tgc	aac	agc	48
Leu	Pro	Ala	Gly	Thr	Arg	Leu	Arg	Arg	Leu	Asp	Val	Ser	Cys	Asn	Ser	
1				5					10					15		

atc	agc	ttc	gtg	gcc	ccc	ggc	ttc	ttt	tcc	aag	gcc	aag	gag	ctg	cga	96
Ile	Ser	Phe	Val	Ala	Pro	Gly	Phe	Phe	Ser	Lys	Ala	Lys	Glu	Leu	Arg	
			20				25						30			

gag	ctc	aac	ctt	agc	gcc	aac	gcc	ctc	aag	aca	gtg	gac	cac	tcc	tgg	144
Glu	Leu	Asn	Leu	Ser	Ala	Asn	Ala	Leu	Lys	Thr	Val	Asp	His	Ser	Trp	
		35					40					45				

ttt	ggg	ccc	ctg	gcg	agt	gcc	ctg	caa	ata	cta	gat	gta	agc	gcc	aac	192
Phe	Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	
	50					55					60					

cct	ctg	cac	tgc	gcc	tgt	ggg	gcg	gcc	ttt	atg	gac	ttc	ctg	ctg	gag	240
Pro	Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	
65					70					75					80	

gtg	cag	gct	gcc	gtg	ccc	ggg	ctg	ccc	agc	cgg	gtg	aag	tgt	ggc	agt	288
Val	Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	
				85					90					95		

ccg	ggc	cag	ctc	cag	ggc	ctc	agc	atc	ttt	gca	cag	gac	ctg	cgc	ctc	336
Pro	Gly	Gln	Leu	Gln	Gly	Leu	Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	
			100					105					110			

tgc	ctg	gat	gag	gcc	ctc	tcc	tgg	gac	tgt	ttc	gcc	ctc	tcg	ctg	ctg	384
Cys	Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	
		115					120					125				

gct	gtg	gct	ctg	ggc	ctg	ggg	gtg	ccc	atg	ctg	cat	cac	ctc	tgt	ggc	432
Ala	Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	
	130					135					140					

tgg	gac	ctc	tgg	tac	tgc	ttc	cac	ctg	tgc	ctg	gcc	tgg	ctt	ccc	tgg	480
Trp	Asp	Leu	Trp	Tyr	Cys	Phe	His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Trp	

145		150		155		160	
cgg ggg cgg caa agt ggg cga gat gag gat gcc ctg ccc tac gat gcc	Arg Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala	165		170		175	528
ttc gtg gtc ttc gac aaa acg cag agc gca gtg gca gac tgg gtg tac	Phe Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr	180		185		190	576
aac gag ctt cgg ggg cag ctg gag gag tgc cgt ggg cgc tgg gca ctc	Asn Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu	195		200		205	624
cgc ctg tgc ctg gag gaa cgc gac tgg ctg cct gcc aaa acc ctc ttt	Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe	210		215		220	672
gag aac ctg tgg gcc tcg gtc tat ggc agc cgc aag acg ctg ttt gtg	Glu Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val	225		230		235	720
ctg gcc cac acg gac cgg gtc agt ggt ctc ttg cgc gcc agc ttc ctg	Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu	245		250		255	768
ctg gcc cag cag cgc ctg ctg gag gac cgc aag gac gtc gtg gtg ctg	Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu	260		265		270	816
gtg atc ctg agc cct gac ggc cgc cgc tcc cgc tac gkg cgg ctg cgc	Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Xaa Arg Leu Arg	275		280		285	864
cag cgc ctc tgc cgc cag agt gtc ctc ctc tgg ccc cac cag ccc agt	Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser	290		295		300	912
ggt cag cgc agc ttc tgg gcc cag ctg ggc atg gcc ctg acc agg gac	Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp	305		310		315	960
aac cac cac ttc tat aac cgg aac ttc tgc cag gga ccc acg gcc gaa	Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu	325		330		335	1008
tagccgtgag ccggaatcct gcacgggtgcc acctccacac tcacctcacc tctgcctgcc							1068
tggtctgacc ctcccctgct cgcctccctc accccacacc tgacacagag caggcactca							1128
ataaatgcta ccgaaggcta aaaaaaaaaa aaaaaaaaaa aanna							1173

<210> 34
<211> 336
<212> PRT
<213> Unknown

<400> 34

Leu	Pro	Ala	Gly	Thr	Arg	Leu	Arg	Arg	Leu	Asp	Val	Ser	Cys	Asn	Ser	
1				5					10					15		
Ile	Ser	Phe	Val	Ala	Pro	Gly	Phe	Phe	Ser	Lys	Ala	Lys	Glu	Leu	Arg	
			20				25						30			
Glu	Leu	Asn	Leu	Ser	Ala	Asn	Ala	Leu	Lys	Thr	Val	Asp	His	Ser	Trp	
		35					40					45				
Phe	Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	
	50					55					60					
Pro	Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	
	65				70					75					80	
Val	Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	
				85					90					95		
Pro	Gly	Gln	Leu	Gln	Gly	Leu	Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	
			100					105					110			
Cys	Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	
		115					120					125				
Ala	Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	
	130					135					140					
Trp	Asp	Leu	Trp	Tyr	Cys	Phe	His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Trp	
145					150					155					160	
Arg	Gly	Arg	Gln	Ser	Gly	Arg	Asp	Glu	Asp	Ala	Leu	Pro	Tyr	Asp	Ala	
				165					170					175		
Phe	Val	Val	Phe	Asp	Lys	Thr	Gln	Ser	Ala	Val	Ala	Asp	Trp	Val	Tyr	
			180					185					190			
Asn	Glu	Leu	Arg	Gly	Gln	Leu	Glu	Glu	Cys	Arg	Gly	Arg	Trp	Ala	Leu	
		195					200					205				
Arg	Leu	Cys	Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Lys	Thr	Leu	Phe	
	210					215					220					
Glu	Asn	Leu	Trp	Ala	Ser	Val	Tyr	Gly	Ser	Arg	Lys	Thr	Leu	Phe	Val	
225					230					235					240	
Leu	Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu	Arg	Ala	Ser	Phe	Leu	
				245					250					255		

Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu
 260 265 270
 Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Xaa Arg Leu Arg
 275 280 285
 Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser
 290 295 300
 Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp
 305 310 315 320
 Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu
 325 330 335

<210> 35
 <211> 497
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:rodent; surmised
 Mus musculus

<400> 35
 tgccccacac ggaccgcgtc agtggcctcc tgcgcaccag cttcctgctg gctcagcagc 60
 gcctgttgga agaccgcaag gacgtggtgg tgttggtgat cctgcgtccg gatgccccac 120
 cgtcccgtta tgtgcgactg cgccagcgtc tctgccgcca gagtgtgctc ttctggcccc 180
 acgagaccaa cgggcagggg ggcttctggg ccagctgag tacagccctg actagggaca 240
 accgccactt ctataaccag aacttctgcc ggggacctac agcagaatag ctcagagcaa 300
 cagctggaaa cagctgcata ttcattgtctg gttcccagat tgctctgcct gccttgctct 360
 gtcttactac accgctatct ggcaagtgcg caatatatgc taccaagcca ccaggccac 420
 ggagcaaagg ttggctgtaa agggtagttt tcttcccatg catctttcag gagagtgaag 480
 atagacacca aaccac 497

<210> 36
 <211> 3099
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

ca	aac	ttg	aaa	aat	ctc	tat	ttg	gcc	tgg	aac	tgc	tat	ttt	aac	aaa	528
le	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn	Cys	Tyr	Phe	Asn	Lys	
	145					150					155					
tt	tgc	gag	aaa	act	aac	ata	gaa	gat	gga	gta	ttt	gaa	acg	ctg	aca	576
al	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly	Val	Phe	Glu	Thr	Leu	Thr	
60					165					170					175	
at	ttg	gag	ttg	cta	tca	cta	tct	ttc	aat	tct	ctt	tca	cat	gtg	cca	624
asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe	Asn	Ser	Leu	Ser	His	Val	Pro	
				180					185					190		
acc	aaa	ctg	cca	agc	tcc	cta	cgc	aaa	ctt	ttt	ctg	agc	aac	acc	cag	672
pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg	Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	
			195					200					205			
atc	aaa	tac	att	agt	gaa	gaa	gat	ttc	aag	gga	ttg	ata	aat	tta	aca	720
ile	Lys	Tyr	Ile	Ser	Glu	Glu	Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	
		210					215					220				
tta	cta	gat	tta	agc	ggg	aac	tgt	ccg	agg	tgc	ttc	aat	gcc	cca	ttt	768
leu	Leu	Asp	Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	
	225					230					235					
cca	ctg	gtg	cct	tgt	gat	ggt	ggt	gct	tca	att	aat	ata	gat	cgt	ttt	816
pro	Cys	Val	Pro	Cys	Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	
240					245					250					255	
gct	ttt	caa	aac	ttg	acc	caa	ctt	cga	tac	cta	aac	ctc	tct	agc	act	864
ala	Phe	Gln	Asn	Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	
				260					265					270		
tcc	ctc	agg	aag	att	aat	gct	gcc	tgg	ttt	aaa	aat	atg	cct	cat	ctg	912
ser	Leu	Arg	Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	
			275					280					285			
aag	gtg	ctg	gat	ctt	gaa	ttc	aac	tat	tta	gtg	gga	gaa	ata	gcc	tct	960
lys	Val	Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Ala	Ser	
		290					295					300				
ggg	gca	ttt	tta	acg	atg	ctg	ccc	cgc	tta	gaa	ata	ctt	gac	ttg	tct	1008
gly	Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser	
	305					310					315					
ttt	aac	tat	ata	aag	ggg	agt	tat	cca	cag	cat	att	aat	att	tcc	aga	1056
phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	Arg	
320					325				330						335	
aac	ttc	tct	aaa	ctt	ttg	tct	cta	cgg	gca	ttg	cat	tta	aga	ggt	tat	1104
asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg	Gly	Tyr	
				340					345					350		

ig al	ttc Phe	cag Gln	gaa Glu	ctc Leu	aga Arg	gaa Glu	gat Asp	gat Asp	ttc Phe	cag Gln	ccc Pro	ctg Leu	atg Met	cag Gln	ctt Leu	1152
			355				360					365				
ca ro	aac Asn	tta Leu	tcg Ser	act Thr	atc Ile	aac Asn	ttg Leu	ggg Gly	att Ile	aat Asn	ttt Phe	att Ile	aag Lys	caa Gln	atc Ile	1200
		370					375					380				
at sp	ttc Phe	aaa Lys	ctt Leu	ttc Phe	caa Gln	aat Asn	ttc Phe	tcc Ser	aat Asn	ctg Leu	gaa Glu	att Ile	att Ile	tac Tyr	ttg Leu	1248
	385					390					395					
ca er 00	gaa Glu	aac Asn	aga Arg	ata Ile	tca Ser	ccg Pro	ttg Leu	gta Val	aaa Lys	gat Asp	acc Thr	cgg Arg	cag Gln	agt Ser	tat Tyr	1296
					405					410					415	
ica ala	aat Asn	agt Ser	tcc Ser	tct Ser	ttt Phe	caa Gln	cgt Arg	cat His	atc Ile	cgg Arg	aaa Lys	cga Arg	cgc Arg	tca Ser	aca Thr	1344
				420					425					430		
gat Asp	ttt Phe	gag Glu	ttt Phe	gac Asp	cca Pro	cat His	tcg Ser	aac Asn	ttt Phe	tat Tyr	cat His	ttc Phe	acc Thr	cgt Arg	cct Pro	1392
	435							440					445			
cta Leu	ata Ile	aag Lys	cca Pro	caa Gln	tgt Cys	gct Ala	gct Ala	tat Tyr	gga Gly	aaa Lys	gcc Ala	tta Leu	gat Asp	tta Leu	agc Ser	1440
	450						455					460				
ctc Leu	aac Asn	agt Ser	att Ile	ttc Phe	ttc Phe	att Ile	ggg Gly	cca Pro	aac Asn	caa Gln	ttt Phe	gaa Glu	aat Asn	ctt Leu	cct Pro	1488
	465					470					475					
gac Asp 480	att Ile	gcc Ala	tgt Cys	tta Leu	aat Asn	ctg Leu	tct Ser	gca Ala	aat Asn	agc Ser	aat Asn	gct Ala	caa Gln	gtg Val	tta Leu	1536
	485									490					495	
agt Ser	gga Gly	act Thr	gaa Glu	ttt Phe	tca Ser	gcc Ala	att Ile	cct Pro	cat His	gtc Val	aaa Lys	tat Tyr	ttg Leu	gat Asp	ttg Leu	1584
				500					505					510		
aca Thr	aac Asn	aat Asn	aga Arg	cta Leu	gac Asp	ttt Phe	gat Asp	aat Asn	gct Ala	agt Ser	gct Ala	ctt Leu	act Thr	gaa Glu	ttg Leu	1632
			515					520					525			
tcc Ser	gac Asp	ttg Leu	gaa Glu	gtt Val	cta Leu	gat Asp	ctc Leu	agc Ser	tat Tyr	aat Asn	tca Ser	cac His	tat Tyr	ttc Phe	aga Arg	1680
		530					535					540				
ata Ile	gca Ala	ggc Gly	gta Val	aca Thr	cat His	cat His	cta Leu	gaa Glu	ttt Phe	att Ile	caa Gln	aat Asn	ttc Phe	aca Thr	aat Asn	1728
	545					550					555					
cta Leu	aaa Lys	gtt Val	tta Leu	aac Asn	ttg Leu	agc Ser	cac His	aac Asn	aac Asn	att Ile	tat Tyr	act Thr	tta Leu	aca Thr	gat Asp	1776

560		565		570		575	
aag tat aac ctg gaa agc aag tcc ctg gta gaa tta gtt ttc agt ggc	1824						
Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly							
		580		585		590	
aat cgc ctt gac att ttg tgg aat gat gat gac aac agg tat atc tcc	1872						
Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg Tyr Ile Ser		595		600		605	
att ttc aaa ggt ctc aag aat ctg aca cgt ctg gat tta tcc ctt aat	1920						
Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp Leu Ser Leu Asn		610		615		620	
agg ctc aag cac atc cca aat gaa gca ttc ctt aat ttg cca gcg agt	1968						
Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu Asn Leu Pro Ala Ser		625		630		635	
ctc act gaa cta cat ata aat gat aat atg tta aag ttt ttt aac tgg	2016						
Leu Thr Glu Leu His Ile Asn Asp Asn Met Leu Lys Phe Phe Asn Trp		640		645		650	655
aca tta ctc cag cag ttt cct cgt ctc gag ttg ctt gac tta cgt gga	2064						
Thr Leu Leu Gln Gln Phe Pro Arg Leu Glu Leu Leu Asp Leu Arg Gly		660		665		670	
aac aaa cta ctc ttt tta act gat agc cta tct gac ttt aca tct tcc	2112						
Asn Lys Leu Leu Phe Leu Thr Asp Ser Leu Ser Asp Phe Thr Ser Ser		675		680		685	
ctt cgg aca ctg ctg ctg agt cat aac agg att tcc cac cta ccc tct	2160						
Leu Arg Thr Leu Leu Leu Ser His Asn Arg Ile Ser His Leu Pro Ser		690		695		700	
ggc ttt ctt tct gaa gtc agt agt ctg aag cac ctc gat tta agt tcc	2208						
Gly Phe Leu Ser Glu Val Ser Ser Leu Lys His Leu Asp Leu Ser Ser		705		710		715	
aat ctg cta aaa aca atm aac aaa tcc gca ctt gaa act aag acc acc	2256						
Asn Leu Leu Lys Thr Xaa Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr		720		725		730	735
acc aaa tta tct atg ttg gaa cta cac gga aac ccc ttt gaa tgc acc	2304						
Thr Lys Leu Ser Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr		740		745		750	
tgt gac att gga gat ttc cga aga tgg atg gat gaa cat ctg aat gtc	2352						
Cys Asp Ile Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val		755		760		765	
aaa att ccc aga ctg gta gat gtc att tgt gcc agt cct ggg gat caa	2400						
Lys Ile Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln		770		775		780	

aga	ggg	aag	agt	att	gtg	agt	ctg	gag	cta	aca	act	tgt	gtt	tca	gat	2448
Arg	Gly	Lys	Ser	Ile	Val	Ser	Leu	Glu	Leu	Thr	Thr	Cys	Val	Ser	Asp	
	785					790					795					
gtc	act	gca	gtg	ata	tta	ttt	ttc	ttc	acg	ttc	ttt	atc	acc	acc	atg	2496
Val	Thr	Ala	Val	Ile	Leu	Phe	Phe	Phe	Thr	Phe	Phe	Ile	Thr	Thr	Met	
	800				805					810					815	
gtt	atg	ttg	gct	gcc	ctg	gct	cac	cat	ttg	ttt	tac	tgg	gat	gtt	tgg	2544
Val	Met	Leu	Ala	Ala	Leu	Ala	His	His	Leu	Phe	Tyr	Trp	Asp	Val	Trp	
				820					825					830		
ttt	ata	tat	aat	gtg	tgt	tta	gct	aag	tta	aaa	ggc	tac	agg	tct	ctt	2592
Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Leu	Lys	Gly	Tyr	Arg	Ser	Leu	
			835					840					845			
tcc	aca	tcc	caa	act	ttc	tat	gat	gct	tac	att	tct	tat	gac	acc	aaa	2640
Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser	Tyr	Asp	Thr	Lys	
		850					855					860				
gat	gcc	tct	gtt	act	gac	tgg	gtg	ata	aat	gag	ctg	cgc	tac	cac	ctt	2688
Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu	Leu	Arg	Tyr	His	Leu	
	865					870					875					
gaa	gag	agc	cga	gac	aaa	aac	gtt	ctc	ctt	tgt	cta	gag	gag	agg	gat	2736
Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu	Cys	Leu	Glu	Glu	Arg	Asp	
	880				885					890					895	
tgg	gac	ccg	gga	ttg	gcc	atc	atc	gac	aac	ctc	atg	cag	agc	atc	aac	2784
Trp	Asp	Pro	Gly	Leu	Ala	Ile	Ile	Asp	Asn	Leu	Met	Gln	Ser	Ile	Asn	
				900					905					910		
caa	agc	aag	aaa	aca	gta	ttt	gtt	tta	acc	aaa	aaa	tat	gca	aaa	agc	2832
Gln	Ser	Lys	Lys	Thr	Val	Phe	Val	Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	
			915					920					925			
tgg	aac	ttt	aaa	aca	gct	ttt	tac	ttg	gcc	ttg	cag	agg	cta	atg	ggc	2880
Trp	Asn	Phe	Lys	Thr	Ala	Phe	Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Gly	
		930					935					940				
gag	aac	atg	gat	gtg	att	ata	ttt	atc	ctg	ctg	gag	cca	gtg	tta	cag	2928
Glu	Asn	Met	Asp	Val	Ile	Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	
	945					950					955					
cat	tct	ccg	tat	ttg	agg	cta	cgg	cag	cgg	atc	tgt	aag	agc	tcc	atc	2976
His	Ser	Pro	Tyr	Leu	Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	
	960				965					970					975	
ctc	cag	tgg	cct	gac	aac	ccg	aag	gca	gaa	ggc	ttg	ttt	tgg	caa	act	3024
Leu	Gln	Trp	Pro	Asp	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr	
				980					985					990		
ctg	aga	aat	gtg	gtc	ttg	act	gaa	aat	gat	tca	cgg	tat	aac	aat	atg	3072

Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met
 995 1000 1005

at gtc gat tcc att aag caa tac taa
 yr Val Asp Ser Ile Lys Gln Tyr
 1010 1015

3099

210> 37
 211> 1032
 212> PRT
 213> Unknown

400> 37
 Met Leu Thr Cys Ile Phe Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys
 -15 -10 -5

Ala Glu Glu Asn Phe Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln
 -1 1 5 10 15

Asn Asp Ser Val Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val
 20 25 30

Pro Gln Thr Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn
 35 40 45

Phe Ile Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu
 50 55 60

Thr Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly
 65 70 75

Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala Phe
 80 85 90 95

Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn Gln Leu
 100 105 110

Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu
 115 120 125

Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu
 130 135 140

Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys Tyr Phe Asn Lys
 145 150 155

Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe Glu Thr Leu Thr
 160 165 170 175

Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu Ser His Val Pro
 180 185 190

190	Lys	Leu	Pro	Ser	Ser	Leu	Arg	Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	
			195					200					205			
205	Le	Lys	Tyr	Ile	Ser	Glu	Glu	Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr
		210						215					220			
220	eu	Leu	Asp	Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe
		225					230					235				
235	ro	Cys	Val	Pro	Cys	Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe
40						245					250					255
255	la	Phe	Gln	Asn	Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr
					260					265					270	
270	er	Leu	Arg	Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu
				275					280					285		
285	ys	Val	Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Ala	Ser
		290						295					300			
300	Gly	Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser
		305					310					315				
315	Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	Arg
320						325					330					335
335	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg	Gly	Tyr
					340					345					350	
350	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	Met	Gln	Leu
				355					360					365		
365	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	Ile	Lys	Gln	Ile
			370					375					380			
380	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	Glu	Ile	Ile	Tyr	Leu
		385					390					395				
395	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	Asp	Thr	Arg	Gln	Ser	Tyr
400						405					410					415
415	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	Ile	Arg	Lys	Arg	Arg	Ser	Thr
					420					425					430	
430	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro
			435						440					445		
445	Leu	Ile	Lys	Pro	Gln	Cys	Ala	Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser
		450					455						460			
460	Leu	Asn	Ser	Ile	Phe	Phe	Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro
		465					470					475				

Asp	Ile	Ala	Cys	Leu	Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	180	485	490	495
Ser	Gly	Thr	Glu	Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	500	505	510	
Thr	Asn	Asn	Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	515	520	525	
Ser	Asp	Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	530	535	540	
Ile	Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	545	550	555	
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	Asp	560	565	570	575
Lys	Tyr	Asn	Leu	Glu	Ser	Lys	Ser	Leu	Val	Glu	Leu	Val	Phe	Ser	Gly	580	585	590	
Asn	Arg	Leu	Asp	Ile	Leu	Trp	Asn	Asp	Asp	Asp	Asn	Arg	Tyr	Ile	Ser	595	600	605	
Ile	Phe	Lys	Gly	Leu	Lys	Asn	Leu	Thr	Arg	Leu	Asp	Leu	Ser	Leu	Asn	610	615	620	
Arg	Leu	Lys	His	Ile	Pro	Asn	Glu	Ala	Phe	Leu	Asn	Leu	Pro	Ala	Ser	625	630	635	
Leu	Thr	Glu	Leu	His	Ile	Asn	Asp	Asn	Met	Leu	Lys	Phe	Phe	Asn	Trp	640	645	650	655
Thr	Leu	Leu	Gln	Gln	Phe	Pro	Arg	Leu	Glu	Leu	Leu	Asp	Leu	Arg	Gly	660	665	670	
Asn	Lys	Leu	Leu	Phe	Leu	Thr	Asp	Ser	Leu	Ser	Asp	Phe	Thr	Ser	Ser	675	680	685	
Leu	Arg	Thr	Leu	Leu	Leu	Ser	His	Asn	Arg	Ile	Ser	His	Leu	Pro	Ser	690	695	700	
Gly	Phe	Leu	Ser	Glu	Val	Ser	Ser	Leu	Lys	His	Leu	Asp	Leu	Ser	Ser	705	710	715	
Asn	Leu	Leu	Lys	Thr	Xaa	Asn	Lys	Ser	Ala	Leu	Glu	Thr	Lys	Thr	Thr	720	725	730	735
Thr	Lys	Leu	Ser	Met	Leu	Glu	Leu	His	Gly	Asn	Pro	Phe	Glu	Cys	Thr	740	745	750	
Cys	Asp	Ile	Gly	Asp	Phe	Arg	Arg	Trp	Met	Asp	Glu	His	Leu	Asn	Val	755	760	765	

Lys Ile Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln
 770 775 780
 Arg Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp
 785 790 795
 Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr Met
 800 805 810 815
 Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp Val Trp
 820 825 830
 Phe Ile Tyr Asn Val Cys Leu Ala Lys Leu Lys Gly Tyr Arg Ser Leu
 835 840 845
 Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys
 850 855 860
 Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu
 865 870 875
 Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp
 880 885 890 895
 Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn
 900 905 910
 Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser
 915 920 925
 Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Gly
 930 935 940
 Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln
 945 950 955
 His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile
 960 965 970 975
 Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr
 980 985 990
 Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met
 995 1000 1005
 Tyr Val Asp Ser Ile Lys Gln Tyr
 1010 1015

<210> 38
 <211> 3046
 <212> DNA
 <213> Unknown

220>
223> Description of Unknown Organism:primate; surmised
Homo sapiens

220>
221> CDS
222> (111)..(2543)

220>
221> mat_peptide
222> (168)..(2543)

400> 38
aatcatcca cgcacctgca gctctgctga gagagtgcaa gccgtggggg ttttgagctc 60

atcttcatca ttcatatgag gaaataagtg gtaaaatcct tggaaataca atg aga 116
Met Arg

ctc atc aga aac att tac ata ttt tgt agt att gtt atg aca gca gag 164
Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr Ala Glu
-15 -10 -5

ggg gat gct cca gag ctg cca gaa gaa agg gaa ctg atg acc aac tgc 212
Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu Met Thr Asn Cys
-1 1 5 10 15

tcc aac atg tct cta aga aag gtt ccc gca gac ttg acc cca gcc aca 260
Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro Ala Thr
20 25 30

acg tca ctg gat tta tcc tat aac ctc ctt ttt caa ctc cag agt tca 308
Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu Phe Gln Leu Gln Ser Ser
35 40 45

gat ttt cat tct gtc tcc aaa ctg aga gtt ttg att cta tgc cat aac 356
Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys His Asn
50 55 60

aga att caa cag ctg gat ctc aaa acc ttt gaa ttc aac aag gag tta 404
Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys Glu Leu
65 70 75

aga tat tta gat ttg tct aat aac aga ctg aag agt gta act tgg tat 452
Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr Trp Tyr
80 85 90 95

tta ctg gca ggt ctc agg tat tta gat ctt tct ttt aat gac ttt gac 500
Leu Leu Ala Gly Leu Arg Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp
100 105 110

acc atg cct atc tgt gag gaa gct ggc aac atg tca cac ctg gaa atc 548
Thr Met Pro Ile Cys Glu Glu Ala Gly Asn Met Ser His Leu Glu Ile

115						120						125						
cta	ggt	ttg	agt	ggg	gca	aaa	ata	caa	aaa	tca	gat	ttc	cag	aaa	att	596		
Leu	Gly	Leu	Ser	Gly	Ala	Lys	Ile	Gln	Lys	Ser	Asp	Phe	Gln	Lys	Ile			
		130					135					140						
gct	cat	ctg	cat	cta	aat	act	gtc	ttc	tta	gga	ttc	aga	act	ctt	cct	644		
Ala	His	Leu	His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr	Leu	Pro			
		145				150					155							
cat	tat	gaa	gaa	ggt	agc	ctg	ccc	atc	tta	aac	aca	aca	aaa	ctg	cac	692		
His	Tyr	Glu	Glu	Gly	Ser	Leu	Pro	Ile	Leu	Asn	Thr	Thr	Lys	Leu	His			
160					165					170					175			
att	gtt	tta	cca	atg	gac	aca	aat	ttc	tgg	gtt	ctt	ttg	cgt	gat	gga	740		
Ile	Val	Leu	Pro	Met	Asp	Thr	Asn	Phe	Trp	Val	Leu	Leu	Arg	Asp	Gly			
				180					185					190				
atc	aag	act	tca	aaa	ata	tta	gaa	atg	aca	aat	ata	gat	ggc	aaa	agc	788		
Ile	Lys	Thr	Ser	Lys	Ile	Leu	Glu	Met	Thr	Asn	Ile	Asp	Gly	Lys	Ser			
			195					200					205					
caa	ttt	gta	agt	tat	gaa	atg	caa	cga	aat	ctt	agt	tta	gaa	aat	gct	836		
Gln	Phe	Val	Ser	Tyr	Glu	Met	Gln	Arg	Asn	Leu	Ser	Leu	Glu	Asn	Ala			
		210					215					220						
aag	aca	tcg	gtt	cta	ttg	ctt	aat	aaa	gtt	gat	tta	ctc	tgg	gac	gac	884		
Lys	Thr	Ser	Val	Leu	Leu	Leu	Asn	Lys	Val	Asp	Leu	Leu	Trp	Asp	Asp			
		225				230					235							
ctt	ttc	ctt	atc	tta	caa	ttt	gtt	tgg	cat	aca	tca	gtg	gaa	cac	ttt	932		
Leu	Phe	Leu	Ile	Leu	Gln	Phe	Val	Trp	His	Thr	Ser	Val	Glu	His	Phe			
240					245					250					255			
cag	atc	cga	aat	gtg	act	ttt	ggg	ggg	aag	gct	tat	ctt	gac	cac	aat	980		
Gln	Ile	Arg	Asn	Val	Thr	Phe	Gly	Gly	Lys	Ala	Tyr	Leu	Asp	His	Asn			
				260					265					270				
tca	ttt	gac	tac	tca	aat	act	gta	atg	aga	act	ata	aaa	ttg	gag	cat	1028		
Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg	Thr	Ile	Lys	Leu	Glu	His			
			275					280					285					
gta	cat	ttc	aga	gtg	ttt	tac	att	caa	cag	gat	aaa	atc	tat	ttg	ctt	1076		
Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln	Gln	Asp	Lys	Ile	Tyr	Leu	Leu			
			290				295					300						
ttg	acc	aaa	atg	gac	ata	gaa	aac	ctg	aca	ata	tca	aat	gca	caa	atg	1124		
Leu	Thr	Lys	Met	Asp	Ile	Glu	Asn	Leu	Thr	Ile	Ser	Asn	Ala	Gln	Met			
		305				310					315							
cca	cac	atg	ctt	ttc	ccg	aat	tat	cct	acg	aaa	ttc	caa	tat	tta	aat	1172		
Pro	His	Met	Leu	Phe	Pro	Asn	Tyr	Pro	Thr	Lys	Phe	Gln	Tyr	Leu	Asn			
320					325					330					335			

ttt gcc aat aat atc tta aca gac gag ttg ttt aaa aga act atc caa	1220
Phe Ala Asn Asn Ile Leu Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln	
340 345 350	
ctg cct cac ttg aaa act ctc att ttg aat ggc aat aaa ctg gag aca	1268
Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr	
355 360 365	
ctt tct tta gta agt tgc ttt gct aac aac aca ccc ttg gaa cac ttg	1316
Leu Ser Leu Val Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu	
370 375 380	
gat ctg agt caa aat cta tta caa cat aaa aat gat gaa aat tgc tca	1364
Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser	
385 390 395	
tgg cca gaa act gtg gtc aat atg aat ctg tca tac aat aaa ttg tct	1412
Trp Pro Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser	
400 405 410 415	
gat tct gtc ttc agg tgc ttg ccc aaa agt att caa ata ctt gac cta	1460
Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu	
420 425 430	
aat aat aac caa atc caa act gta cct aaa gag act att cat ctg atg	1508
Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu Met	
435 440 445	
gcc tta cga gaa cta aat att gca ttt aat ttt cta act gat ctc cct	1556
Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp Leu Pro	
450 455 460	
gga tgc agt cat ttc agt aga ctt tca gtt ctg aac att gaa atg aac	1604
Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu Met Asn	
465 470 475	
ttc att ctc agc cca tct ctg gat ttt gtt cag agc tgc cag gaa gtt	1652
Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser Cys Gln Glu Val	
480 485 490 495	
aaa act cta aat gcg gga aga aat cca ttc cgg tgt acc tgt gaa tta	1700
Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys Glu Leu	
500 505 510	
aaa aat ttc att cag ctt gaa aca tat tca gag gtc atg atg gtt gga	1748
Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser Glu Val Met Met Val Gly	
515 520 525	
tgg tca gat tca tac acc tgt gaa tac cct tta aac cta agg gga act	1796
Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly Thr	
530 535 540	
agg tta aaa gac gtt cat ctc cac gaa tta tct tgc aac aca gct ctg	1844

Arg	Leu	Lys	Asp	Val	His	Leu	His	Glu	Leu	Ser	Cys	Asn	Thr	Ala	Leu	
545						550					555					
ttg	att	gtc	acc	att	gtg	gtt	att	atg	cta	gtt	ctg	ggg	ttg	gct	gtg	1892
Leu	Ile	Val	Thr	Ile	Val	Val	Ile	Met	Leu	Val	Leu	Gly	Leu	Ala	Val	
560					565				570						575	
gcc	ttc	tgc	tgt	ctc	cac	ttt	gat	ctg	ccc	tgg	tat	ctc	agg	atg	cta	1940
Ala	Phe	Cys	Cys	Leu	His	Phe	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Leu	
				580					585					590		
ggt	caa	tgc	aca	caa	aca	tgg	cac	agg	gtt	agg	aaa	aca	acc	caa	gaa	1988
Gly	Gln	Cys	Thr	Gln	Thr	Trp	His	Arg	Val	Arg	Lys	Thr	Thr	Gln	Glu	
			595					600					605			
caa	ctc	aag	aga	aat	gtc	cga	ttc	cac	gca	ttt	att	tca	tac	agt	gaa	2036
Gln	Leu	Lys	Arg	Asn	Val	Arg	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu	
		610					615					620				
cat	gat	tct	ctg	tgg	gtg	aag	aat	gaa	ttg	atc	ccc	aat	cta	gag	aag	2084
His	Asp	Ser	Leu	Trp	Val	Lys	Asn	Glu	Leu	Ile	Pro	Asn	Leu	Glu	Lys	
						630					635					
gaa	gat	ggt	tct	atc	ttg	att	tgc	ctt	tat	gaa	agc	tac	ttt	gac	cct	2132
Glu	Asp	Gly	Ser	Ile	Leu	Ile	Cys	Leu	Tyr	Glu	Ser	Tyr	Phe	Asp	Pro	
640					645					650					655	
ggc	aaa	agc	att	agt	gaa	aat	att	gta	agc	ttc	att	gag	aaa	agc	tat	2180
Gly	Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys	Ser	Tyr	
				660					665					670		
aag	tcc	atc	ttt	gtt	ttg	tct	ccc	aac	ttt	gtc	cag	aat	gag	tgg	tgc	2228
Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu	Trp	Cys	
			675					680					685			
cat	tat	gaa	ttc	tac	ttt	gcc	cac	cac	aat	ctc	ttc	cat	gaa	aat	tct	2276
His	Tyr	Glu	Phe	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	Asn	Ser	
		690					695					700				
gat	cat	ata	att	ctt	atc	tta	ctg	gaa	ccc	att	cca	ttc	tat	tgc	att	2324
Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe	Tyr	Cys	Ile	
						710					715					
ccc	acc	agg	tat	cat	aaa	ctg	aaa	gct	ctc	ctg	gaa	aaa	aaa	gca	tac	2372
Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu	Lys	Lys	Ala	Tyr	
720					725					730					735	
ttg	gaa	tgg	ccc	aag	gat	agg	cgt	aaa	tgt	ggg	ctt	ttc	tgg	gca	aac	2420
Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly	Leu	Phe	Trp	Ala	Asn	
				740					745					750		
ctt	cga	gct	gct	att	aat	gtt	aat	gta	tta	gcc	acc	aga	gaa	atg	tat	2468
Leu	Arg	Ala	Ala	Ile	Asn	Val	Asn	Val	Leu	Ala	Thr	Arg	Glu	Met	Tyr	
			755					760					765			

jaa ctg cag aca ttc aca gag tta aat gaa gag tct cga ggt tct aca 2516
 glul Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser Thr
 770 775 780

atc tct ctg atg aga aca gat tgt cta taaaatccca cagtccttgg 2563
 ile Ser Leu Met Arg Thr Asp Cys Leu
 785 790

gaagttgggg accacataca ctgttgggat gtacattgat acaaccttta tgatggcaat 2623
 ttgacaatat ttattaaaat aaaaaatggt tattcccttc atatcagttt ctagaaggat 2683
 ttctaagaat gtatcctata gaaacacctt cacaagttaa taagggctta tggaaaaagg 2743
 tgttcacccc aggattgttt ataatcatga aaaatgtggc caggtgcagt ggctcactct 2803
 tgtaatccca gcactatggg aggccaagggt gggtgaccca cgaggtcaag agatggagac 2863
 catcctggcc aacatggtga aaccctgtct ctactaaaaa taaaaaatt agctgggcgt 2923
 gatggtgcac gcctgtagtc ccagctactt gggaggctga ggcaggagaa tcgcttgaac 2983
 ccggaggtg gcagttgcag tgagctgaga tcgagccact gcactccagc ctggtgacag 3043
 agc 3046

<210> 39
 <211> 811
 <212> PRT
 <213> Unknown

<400> 39
 Met Arg Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr
 -15 -10 -5

Ala Glu Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu Met Thr
 -1 1 5 10

Asn Cys Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro
 15 20 25

Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu Phe Gln Leu Gln
 30 35 40 45

Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys
 50 55 60

His Asn Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys
 65 70 75

Glu Leu Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr

80

85

90

Trp	Tyr	Leu	Leu	Ala	Gly	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Phe	Asn	Asp
	95					100					105				
Phe	Asp	Thr	Met	Pro	Ile	Cys	Glu	Glu	Ala	Gly	Asn	Met	Ser	His	Leu
110					115					120					125
Glu	Ile	Leu	Gly	Leu	Ser	Gly	Ala	Lys	Ile	Gln	Lys	Ser	Asp	Phe	Gln
				130					135					140	
Lys	Ile	Ala	His	Leu	His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr
			145					150					155		
Leu	Pro	His	Tyr	Glu	Glu	Gly	Ser	Leu	Pro	Ile	Leu	Asn	Thr	Thr	Lys
		160					165					170			
Leu	His	Ile	Val	Leu	Pro	Met	Asp	Thr	Asn	Phe	Trp	Val	Leu	Leu	Arg
	175					180					185				
Asp	Gly	Ile	Lys	Thr	Ser	Lys	Ile	Leu	Glu	Met	Thr	Asn	Ile	Asp	Gly
190					195					200					205
Lys	Ser	Gln	Phe	Val	Ser	Tyr	Glu	Met	Gln	Arg	Asn	Leu	Ser	Leu	Glu
				210					215					220	
Asn	Ala	Lys	Thr	Ser	Val	Leu	Leu	Leu	Asn	Lys	Val	Asp	Leu	Leu	Trp
			225					230					235		
Asp	Asp	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Val	Trp	His	Thr	Ser	Val	Glu
		240					245					250			
His	Phe	Gln	Ile	Arg	Asn	Val	Thr	Phe	Gly	Gly	Lys	Ala	Tyr	Leu	Asp
	255					260					265				
His	Asn	Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg	Thr	Ile	Lys	Leu
270					275					280					285
Glu	His	Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln	Gln	Asp	Lys	Ile	Tyr
			290						295					300	
Leu	Leu	Leu	Thr	Lys	Met	Asp	Ile	Glu	Asn	Leu	Thr	Ile	Ser	Asn	Ala
			305					310					315		
Gln	Met	Pro	His	Met	Leu	Phe	Pro	Asn	Tyr	Pro	Thr	Lys	Phe	Gln	Tyr
		320					325					330			
Leu	Asn	Phe	Ala	Asn	Asn	Ile	Leu	Thr	Asp	Glu	Leu	Phe	Lys	Arg	Thr
	335					340					345				
Ile	Gln	Leu	Pro	His	Leu	Lys	Thr	Leu	Ile	Leu	Asn	Gly	Asn	Lys	Leu
350					355					360					365
Glu	Thr	Leu	Ser	Leu	Val	Ser	Cys	Phe	Ala	Asn	Asn	Thr	Pro	Leu	Glu

370								375				380			
His	Leu	Asp	Leu	Ser	Gln	Asn	Leu	Leu	Gln	His	Lys	Asn	Asp	Glu	Asn
			385					390					395		
Cys	Ser	Trp	Pro	Glu	Thr	Val	Val	Asn	Met	Asn	Leu	Ser	Tyr	Asn	Lys
		400					405					410			
Leu	Ser	Asp	Ser	Val	Phe	Arg	Cys	Leu	Pro	Lys	Ser	Ile	Gln	Ile	Leu
	415					420					425				
Asp	Leu	Asn	Asn	Asn	Gln	Ile	Gln	Thr	Val	Pro	Lys	Glu	Thr	Ile	His
430					435					440					445
Leu	Met	Ala	Leu	Arg	Glu	Leu	Asn	Ile	Ala	Phe	Asn	Phe	Leu	Thr	Asp
				450					455					460	
Leu	Pro	Gly	Cys	Ser	His	Phe	Ser	Arg	Leu	Ser	Val	Leu	Asn	Ile	Glu
			465						470				475		
Met	Asn	Phe	Ile	Leu	Ser	Pro	Ser	Leu	Asp	Phe	Val	Gln	Ser	Cys	Gln
	480						485					490			
Glu	Val	Lys	Thr	Leu	Asn	Ala	Gly	Arg	Asn	Pro	Phe	Arg	Cys	Thr	Cys
495						500					505				
Glu	Leu	Lys	Asn	Phe	Ile	Gln	Leu	Glu	Thr	Tyr	Ser	Glu	Val	Met	Met
510					515					520					525
Val	Gly	Trp	Ser	Asp	Ser	Tyr	Thr	Cys	Glu	Tyr	Pro	Leu	Asn	Leu	Arg
				530					535					540	
Gly	Thr	Arg	Leu	Lys	Asp	Val	His	Leu	His	Glu	Leu	Ser	Cys	Asn	Thr
			545					550					555		
Ala	Leu	Leu	Ile	Val	Thr	Ile	Val	Val	Ile	Met	Leu	Val	Leu	Gly	Leu
		560					565					570			
Ala	Val	Ala	Phe	Cys	Cys	Leu	His	Phe	Asp	Leu	Pro	Trp	Tyr	Leu	Arg
	575					580					585				
Met	Leu	Gly	Gln	Cys	Thr	Gln	Thr	Trp	His	Arg	Val	Arg	Lys	Thr	Thr
590					595					600					605
Gln	Glu	Gln	Leu	Lys	Arg	Asn	Val	Arg	Phe	His	Ala	Phe	Ile	Ser	Tyr
				610					615					620	
Ser	Glu	His	Asp	Ser	Leu	Trp	Val	Lys	Asn	Glu	Leu	Ile	Pro	Asn	Leu
			625						630				635		
Glu	Lys	Glu	Asp	Gly	Ser	Ile	Leu	Ile	Cys	Leu	Tyr	Glu	Ser	Tyr	Phe
		640					645					650			

Asp	Pro	Gly	Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys
655						660					665				
Ser	Tyr	Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu
670					675					680					685
Trp	Cys	His	Tyr	Glu	Phe	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu
				690					695					700	
Asn	Ser	Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe	Tyr
			705					710					715		
Cys	Ile	Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu	Lys	Lys
		720					725					730			
Ala	Tyr	Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly	Leu	Phe	Trp
735						740					745				
Ala	Asn	Leu	Arg	Ala	Ala	Ile	Asn	Val	Asn	Val	Leu	Ala	Thr	Arg	Glu
750					755					760					765
Met	Tyr	Glu	Leu	Gln	Thr	Phe	Thr	Glu	Leu	Asn	Glu	Glu	Ser	Arg	Gly
				770					775					780	
Ser	Thr	Ile	Ser	Leu	Met	Arg	Thr	Asp	Cys	Leu					
			785					790							

<210> 40

<211> 2760

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (68)..(2455)

<220>

<221> mat_peptide

<222> (161)..(2455)

<220>

<221> misc_feature

<222> (2529)

<223> n may be a, c, g, or t

<400> 40

aagaatttgg actcatatca agatgctctg aagaagaaca accctttagg atagccactg 60

caacatc atg acc aaa gac aaa gaa cct att gtt aaa agc ttc cat ttt 109

Met Thr Lys Asp Lys Glu Pro Ile Val Lys Ser Phe His Phe
 -30 -25 -20

gtt tgc ctt atg atc ata ata gtt gga acc aga atc cag ttc tcc gac 157
 Val Cys Leu Met Ile Ile Ile Val Gly Thr Arg Ile Gln Phe Ser Asp
 -15 -10 -5

gga aat gaa ttt gca gta gac aag tca aaa aga ggt ctt att cat gtt 205
 Gly Asn Glu Phe Ala Val Asp Lys Ser Lys Arg Gly Leu Ile His Val
 -1 1 5 10 15

cca aaa gac cta ccg ctg aaa acc aaa gtc tta gat atg tct cag aac 253
 Pro Lys Asp Leu Pro Leu Lys Thr Lys Val Leu Asp Met Ser Gln Asn
 20 25 30

tac atc gct gag ctt cag gtc tct gac atg agc ttt cta tca gag ttg 301
 Tyr Ile Ala Glu Leu Gln Val Ser Asp Met Ser Phe Leu Ser Glu Leu
 35 40 45

aca gtt ttg aga ctt tcc cat aac aga atc cag cta ctt gat tta agt 349
 Thr Val Leu Arg Leu Ser His Asn Arg Ile Gln Leu Leu Asp Leu Ser
 50 55 60

gtt ttc aag ttc aac cag gat tta gaa tat ttg gat tta tct cat aat 397
 Val Phe Lys Phe Asn Gln Asp Leu Glu Tyr Leu Asp Leu Ser His Asn
 65 70 75

cag ttg caa aag ata tcc tgc cat cct att gtg agt ttc agg cat tta 445
 Gln Leu Gln Lys Ile Ser Cys His Pro Ile Val Ser Phe Arg His Leu
 80 85 90 95

gat ttc tca ttc aat gat ttc aag gcc ctg ccc atc tgt aag gaa ttt 493
 Asp Leu Ser Phe Asn Asp Phe Lys Ala Leu Pro Ile Cys Lys Glu Phe
 100 105 110

ggc aac tta tca caa ctg aat ttc ttg gga ttg agt gct atg aag ctg 541
 Gly Asn Leu Ser Gln Leu Asn Phe Leu Gly Leu Ser Ala Met Lys Leu
 115 120 125

caa aaa tta gat ttg ctg cca att gct cac ttg cat cta agt tat atc 589
 Gln Lys Leu Asp Leu Leu Pro Ile Ala His Leu His Leu Ser Tyr Ile
 130 135 140

ctt ctg gat tta aga aat tat tat ata aaa gaa aat gag aca gaa agt 637
 Leu Leu Asp Leu Arg Asn Tyr Tyr Ile Lys Glu Asn Glu Thr Glu Ser
 145 150 155

cta caa att ctg aat gca aaa acc ctt cac ctt gtt ttt cac cca act 685
 Leu Gln Ile Leu Asn Ala Lys Thr Leu His Leu Val Phe His Pro Thr
 160 165 170 175

agt tta ttc gct atc caa gtg aac ata tca gtt aat act tta ggg tgc 733
 Ser Leu Phe Ala Ile Gln Val Asn Ile Ser Val Asn Thr Leu Gly Cys

180

185

190

ta	caa	ctg	act	aat	att	aaa	ttg	aat	gat	gac	aac	tgt	caa	gtt	ttc	781
eu	Gln	Leu	Thr	Asn	Ile	Lys	Leu	Asn	Asp	Asp	Asn	Cys	Gln	Val	Phe	
			195					200					205			

tt	aaa	ttt	tta	tca	gaa	ctc	acc	aga	ggc	cca	acc	tta	ctg	aat	ttt	829
le	Lys	Phe	Leu	Ser	Glu	Leu	Thr	Arg	Gly	Pro	Thr	Leu	Leu	Asn	Phe	
		210					215					220				

acc	ctc	aac	cac	ata	gaa	acg	act	tgg	aaa	tgc	ctg	gtc	aga	gtc	ttt	877
thr	Leu	Asn	His	Ile	Glu	Thr	Thr	Trp	Lys	Cys	Leu	Val	Arg	Val	Phe	
	225					230					235					

caa	ttt	ctt	tgg	ccc	aaa	cct	gtg	gaa	tat	ctc	aat	att	tac	aat	tta	925
gln	Phe	Leu	Trp	Pro	Lys	Pro	Val	Glu	Tyr	Leu	Asn	Ile	Tyr	Asn	Leu	
240					245					250					255	

aca	ata	att	gaa	agc	att	cgt	gaa	gaa	gat	ttt	act	tat	tct	aaa	acg	973
Thr	Ile	Ile	Glu	Ser	Ile	Arg	Glu	Glu	Asp	Phe	Thr	Tyr	Ser	Lys	Thr	
				260					265						270	

aca	ttg	aaa	gca	ttg	aca	ata	gaa	cat	atc	acg	aac	caa	gtt	ttt	ctg	1021
Thr	Leu	Lys	Ala	Leu	Thr	Ile	Glu	His	Ile	Thr	Asn	Gln	Val	Phe	Leu	
			275					280					285			

ttt	tca	cag	aca	gct	ttg	tac	acc	gtg	ttt	tct	gag	atg	aac	att	atg	1069
Phe	Ser	Gln	Thr	Ala	Leu	Tyr	Thr	Val	Phe	Ser	Glu	Met	Asn	Ile	Met	
		290					295					300				

atg	tta	acc	att	tca	gat	aca	cct	ttt	ata	cac	atg	ctg	tgt	cct	cat	1117
Met	Leu	Thr	Ile	Ser	Asp	Thr	Pro	Phe	Ile	His	Met	Leu	Cys	Pro	His	
						310					315					

gca	tca	agc	aca	ttc	aag	ttt	ttg	aac	ttt	acc	cag	aac	gtt	ttc	aca	1165
Ala	Pro	Ser	Thr	Phe	Lys	Phe	Leu	Asn	Phe	Thr	Gln	Asn	Val	Phe	Thr	
320					325					330					335	

gat	agt	att	ttt	gaa	aaa	tgt	tcc	acg	tta	gtt	aaa	ttg	gag	aca	ctt	1213
Asp	Ser	Ile	Phe	Glu	Lys	Cys	Ser	Thr	Leu	Val	Lys	Leu	Glu	Thr	Leu	
				340					345					350		

atc	tta	caa	aag	aat	gga	tta	aaa	gac	ctt	ttc	aaa	gta	ggc	ctc	atg	1261
Ile	Leu	Gln	Lys	Asn	Gly	Leu	Lys	Asp	Leu	Phe	Lys	Val	Gly	Leu	Met	
			355					360					365			

acg	aag	gat	atg	cct	tct	ttg	gaa	ata	ctg	gat	gtt	agc	tgg	aat	tct	1309
Thr	Lys	Asp	Met	Pro	Ser	Leu	Glu	Ile	Leu	Asp	Val	Ser	Trp	Asn	Ser	
		370					375					380				

ttg	gaa	tct	ggc	aga	cat	aaa	gaa	aac	tgc	act	tgg	gtt	gag	agt	ata	1357
Leu	Glu	Ser	Gly	Arg	His	Lys	Glu	Asn	Cys	Thr	Trp	Val	Glu	Ser	Ile	
	385					390					395					

gtg	gtg	tta	aat	ttg	tct	tca	aat	atg	ctt	act	gac	tct	gtt	ttc	aga	1405
Val	Val	Leu	Asn	Leu	Ser	Ser	Asn	Met	Leu	Thr	Asp	Ser	Val	Phe	Arg	
400					405					410					415	
tgt	tta	cct	ccc	agg	atc	aag	gta	ctt	gat	ctt	cac	agc	aat	aaa	ata	1453
Cys	Leu	Pro	Pro	Arg	Ile	Lys	Val	Leu	Asp	Leu	His	Ser	Asn	Lys	Ile	
				420					425					430		
aag	agc	gtt	cct	aaa	caa	gtc	gta	aaa	ctg	gaa	gct	ttg	caa	gaa	ctc	1501
Lys	Ser	Val	Pro	Lys	Gln	Val	Val	Lys	Leu	Glu	Ala	Leu	Gln	Glu	Leu	
			435					440					445			
aat	gtt	gct	ttc	aat	tct	tta	act	gac	ctt	cct	gga	tgt	ggc	agc	ttt	1549
Asn	Val	Ala	Phe	Asn	Ser	Leu	Thr	Asp	Leu	Pro	Gly	Cys	Gly	Ser	Phe	
		450					455					460				
agc	agc	ctt	tct	gta	ttg	atc	att	gat	cac	aat	tca	gtt	tcc	cac	cca	1597
Ser	Ser	Leu	Ser	Val	Leu	Ile	Ile	Asp	His	Asn	Ser	Val	Ser	His	Pro	
	465					470					475					
tcg	gct	gat	ttc	ttc	cag	agc	tgc	cag	aag	atg	agg	tca	ata	aaa	gca	1645
Ser	Ala	Asp	Phe	Phe	Gln	Ser	Cys	Gln	Lys	Met	Arg	Ser	Ile	Lys	Ala	
480					485					490					495	
ggg	gac	aat	cca	ttc	caa	tgt	acc	tgt	gag	cta	aga	gaa	ttt	gtc	aaa	1693
Gly	Asp	Asn	Pro	Phe	Gln	Cys	Thr	Cys	Glu	Leu	Arg	Glu	Phe	Val	Lys	
			500						505					510		
aat	ata	gac	caa	gta	tca	agt	gaa	gtg	tta	gag	ggc	tgg	cct	gat	tct	1741
Asn	Ile	Asp	Gln	Val	Ser	Ser	Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	
			515					520					525			
tat	aag	tgt	gac	tac	cca	gaa	agt	tat	aga	gga	agc	cca	cta	aag	gac	1789
Tyr	Lys	Cys	Asp	Tyr	Pro	Glu	Ser	Tyr	Arg	Gly	Ser	Pro	Leu	Lys	Asp	
		530					535					540				
ttt	cac	atg	tct	gaa	tta	tcc	tgc	aac	ata	act	ctg	ctg	atc	gtc	acc	1837
Phe	His	Met	Ser	Glu	Leu	Ser	Cys	Asn	Ile	Thr	Leu	Leu	Ile	Val	Thr	
	545					550					555					
atc	ggt	gcc	acc	atg	ctg	gtg	ttg	gct	gtg	act	gtg	acc	tcc	ctc	tgc	1885
Ile	Gly	Ala	Thr	Met	Leu	Val	Leu	Ala	Val	Thr	Val	Thr	Ser	Leu	Cys	
	560				565					570					575	
atc	tac	ttg	gat	ctg	ccc	tgg	tat	ctc	agg	atg	gtg	tgc	cag	tgg	acc	1933
Ile	Tyr	Leu	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Val	Cys	Gln	Trp	Thr	
			580						585					590		
cag	act	cgg	cgc	agg	gcc	agg	aac	ata	ccc	tta	gaa	gaa	ctc	caa	aga	1981
Gln	Thr	Arg	Arg	Arg	Ala	Arg	Asn	Ile	Pro	Leu	Glu	Glu	Leu	Gln	Arg	
			595					600					605			
aac	ctc	cag	ttt	cat	gct	ttt	att	tca	tat	agt	gaa	cat	gat	tct	gcc	2029

Asn	Leu	Gln	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu	His	Asp	Ser	Ala		
		610					615					620					
tgg	gtg	aaa	agt	gaa	ttg	gta	cct	tac	cta	gaa	aaa	gaa	gat	ata	cag	2077	
Trp	Val	Lys	Ser	Glu	Leu	Val	Pro	Tyr	Leu	Glu	Lys	Glu	Asp	Ile	Gln		
		625				630					635						
att	tgt	ctt	cat	gag	agg	aac	ttt	gtc	cct	ggc	aag	agc	att	gtg	gaa	2125	
Ile	Cys	Leu	His	Glu	Arg	Asn	Phe	Val	Pro	Gly	Lys	Ser	Ile	Val	Glu		
		640			645					650					655		
aat	atc	atc	aac	tgc	att	gag	aag	agt	tac	aag	tcc	atc	ttt	gtt	ttg	2173	
Asn	Ile	Ile	Asn	Cys	Ile	Glu	Lys	Ser	Tyr	Lys	Ser	Ile	Phe	Val	Leu		
				660					665					670			
tct	ccc	aac	ttt	gtc	cag	agt	gag	tgg	tgc	cat	tac	gaa	ctc	tat	ttt	2221	
Ser	Pro	Asn	Phe	Val	Gln	Ser	Glu	Trp	Cys	His	Tyr	Glu	Leu	Tyr	Phe		
			675					680					685				
gcc	cat	cac	aat	ctc	ttt	cat	gaa	gga	tct	aat	aac	tta	atc	ctc	atc	2269	
Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn	Asn	Leu	Ile	Leu	Ile		
			690				695					700					
tta	ctg	gaa	ccc	att	cca	cag	aac	agc	att	ccc	aac	aag	tac	cac	aag	2317	
Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile	Pro	Asn	Lys	Tyr	His	Lys		
		705				710					715						
ctg	aag	gct	ctc	atg	acg	cag	cgg	act	tat	ttg	cag	tgg	ccc	aag	gag	2365	
Leu	Lys	Ala	Leu	Met	Thr	Gln	Arg	Thr	Tyr	Leu	Gln	Trp	Pro	Lys	Glu		
					725					730					735		
aaa	agc	aaa	cgt	ggg	ctc	ttt	tgg	gct	aac	att	aga	gcc	gct	ttt	aat	2413	
Lys	Ser	Lys	Arg	Gly	Leu	Phe	Trp	Ala	Asn	Ile	Arg	Ala	Ala	Phe	Asn		
				740					745					750			
atg	aaa	tta	aca	cta	gtc	act	gaa	aac	aat	gat	gtg	aaa	tct			2455	
Met	Lys	Leu	Thr	Leu	Val	Thr	Glu	Asn	Asn	Asp	Val	Lys	Ser				
			755				760						765				
taaaaaaatt taggaaattc aacttaagaa accattatattt acttggatga tgggtgaatag																2515	
tacagtcgta agtnactgtc tggaggtgcc tccattatcc tcatgccttc aggaaagact																2575	
taacaaaaaac aatgtttcat ctgggggaact gagctaggcg gtgagggttag cctgccagtt																2635	
agagacagcc cagtctcttc tggttttaatc attatgtttc aaattgaaac agtctctttt																2695	
gagtaaattgc tcagtttttc agctcctctc cactctgctt tcccaaattgg attctgttgg																2755	
tgaag																2760	

<210> 41
<211> 796

<212> PRT
<213> Unknown

<400> 41

Met	Thr	Lys	Asp	Lys	Glu	Pro	Ile	Val	Lys	Ser	Phe	His	Phe	Val	Cys
-30						-25					-20				
Leu	Met	Ile	Ile	Ile	Val	Gly	Thr	Arg	Ile	Gln	Phe	Ser	Asp	Gly	Asn
-15					-10					-5				-1	1
Glu	Phe	Ala	Val	Asp	Lys	Ser	Lys	Arg	Gly	Leu	Ile	His	Val	Pro	Lys
			5					10					15		
Asp	Leu	Pro	Leu	Lys	Thr	Lys	Val	Leu	Asp	Met	Ser	Gln	Asn	Tyr	Ile
		20					25					30			
Ala	Glu	Leu	Gln	Val	Ser	Asp	Met	Ser	Phe	Leu	Ser	Glu	Leu	Thr	Val
	35					40					45				
Leu	Arg	Leu	Ser	His	Asn	Arg	Ile	Gln	Leu	Leu	Asp	Leu	Ser	Val	Phe
50					55					60					65
Lys	Phe	Asn	Gln	Asp	Leu	Glu	Tyr	Leu	Asp	Leu	Ser	His	Asn	Gln	Leu
				70					75					80	
Gln	Lys	Ile	Ser	Cys	His	Pro	Ile	Val	Ser	Phe	Arg	His	Leu	Asp	Leu
			85					90					95		
Ser	Phe	Asn	Asp	Phe	Lys	Ala	Leu	Pro	Ile	Cys	Lys	Glu	Phe	Gly	Asn
		100					105					110			
Leu	Ser	Gln	Leu	Asn	Phe	Leu	Gly	Leu	Ser	Ala	Met	Lys	Leu	Gln	Lys
	115					120					125				
Leu	Asp	Leu	Leu	Pro	Ile	Ala	His	Leu	His	Leu	Ser	Tyr	Ile	Leu	Leu
-130					135					140					145
Asp	Leu	Arg	Asn	Tyr	Tyr	Ile	Lys	Glu	Asn	Glu	Thr	Glu	Ser	Leu	Gln
				150					155					160	
Ile	Leu	Asn	Ala	Lys	Thr	Leu	His	Leu	Val	Phe	His	Pro	Thr	Ser	Leu
			165					170					175		
Phe	Ala	Ile	Gln	Val	Asn	Ile	Ser	Val	Asn	Thr	Leu	Gly	Cys	Leu	Gln
		180					185					190			
Leu	Thr	Asn	Ile	Lys	Leu	Asn	Asp	Asp	Asn	Cys	Gln	Val	Phe	Ile	Lys
	195					200					205				
Phe	Leu	Ser	Glu	Leu	Thr	Arg	Gly	Pro	Thr	Leu	Leu	Asn	Phe	Thr	Leu
210					215					220					225
Asn	His	Ile	Glu	Thr	Thr	Trp	Lys	Cys	Leu	Val	Arg	Val	Phe	Gln	Phe

230						235						240					
Leu	Trp	Pro	Lys	Pro	Val	Glu	Tyr	Leu	Asn	Ile	Tyr	Asn	Leu	Thr	Ile		
			245					250					255				
Ile	Glu	Ser	Ile	Arg	Glu	Glu	Asp	Phe	Thr	Tyr	Ser	Lys	Thr	Thr	Leu		
		260				265						270					
Lys	Ala	Leu	Thr	Ile	Glu	His	Ile	Thr	Asn	Gln	Val	Phe	Leu	Phe	Ser		
	275				280						285						
Gln	Thr	Ala	Leu	Tyr	Thr	Val	Phe	Ser	Glu	Met	Asn	Ile	Met	Met	Leu		
290					295					300					305		
Thr	Ile	Ser	Asp	Thr	Pro	Phe	Ile	His	Met	Leu	Cys	Pro	His	Ala	Pro		
				310					315					320			
Ser	Thr	Phe	Lys	Phe	Leu	Asn	Phe	Thr	Gln	Asn	Val	Phe	Thr	Asp	Ser		
			325					330					335				
Ile	Phe	Glu	Lys	Cys	Ser	Thr	Leu	Val	Lys	Leu	Glu	Thr	Leu	Ile	Leu		
		340				345						350					
Gln	Lys	Asn	Gly	Leu	Lys	Asp	Leu	Phe	Lys	Val	Gly	Leu	Met	Thr	Lys		
	355					360					365						
Asp	Met	Pro	Ser	Leu	Glu	Ile	Leu	Asp	Val	Ser	Trp	Asn	Ser	Leu	Glu		
370					375					380					385		
Ser	Gly	Arg	His	Lys	Glu	Asn	Cys	Thr	Trp	Val	Glu	Ser	Ile	Val	Val		
				390					395					400			
Leu	Asn	Leu	Ser	Ser	Asn	Met	Leu	Thr	Asp	Ser	Val	Phe	Arg	Cys	Leu		
			405					410					415				
Pro	Pro	Arg	Ile	Lys	Val	Leu	Asp	Leu	His	Ser	Asn	Lys	Ile	Lys	Ser		
		420				425						430					
Val	Pro	Lys	Gln	Val	Val	Lys	Leu	Glu	Ala	Leu	Gln	Glu	Leu	Asn	Val		
	435					440					445						
Ala	Phe	Asn	Ser	Leu	Thr	Asp	Leu	Pro	Gly	Cys	Gly	Ser	Phe	Ser	Ser		
450					455					460					465		
Leu	Ser	Val	Leu	Ile	Ile	Asp	His	Asn	Ser	Val	Ser	His	Pro	Ser	Ala		
				470					475					480			
Asp	Phe	Phe	Gln	Ser	Cys	Gln	Lys	Met	Arg	Ser	Ile	Lys	Ala	Gly	Asp		
			485					490					495				
Asn	Pro	Phe	Gln	Cys	Thr	Cys	Glu	Leu	Arg	Glu	Phe	Val	Lys	Asn	Ile		
		500					505					510					
Asp	Gln	Val	Ser	Ser	Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	Tyr	Lys		

515

520

525

Cys Asp Tyr Pro Glu Ser Tyr Arg Gly Ser Pro Leu Lys Asp Phe His
530 535 540 545

Met Ser Glu Leu Ser Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Gly
550 555 560

Ala Thr Met Leu Val Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr
565 570 575

Leu Asp Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr
580 585 590

Arg Arg Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu
595 600 605

Gln Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser Ala Trp Val
610 615 620 625

Lys Ser Glu Leu Val Pro Tyr Leu Glu Lys Glu Asp Ile Gln Ile Cys
630 635 640

Leu His Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile
645 650 655

Ile Asn Cys Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro
660 665 670

Asn Phe Val Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His
675 680 685

His Asn Leu Phe His Glu Gly Ser Asn Asn Leu Ile Leu Ile Leu Leu
690 695 700 705

Glu Pro Ile Pro Gln Asn Ser Ile Pro Asn Lys Tyr His Lys Leu Lys
710 715 720

Ala Leu Met Thr Gln Arg Thr Tyr Leu Gln Trp Pro Lys Glu Lys Ser
725 730 735

Lys Arg Gly Leu Phe Trp Ala Asn Ile Arg Ala Ala Phe Asn Met Lys
740 745 750

Leu Thr Leu Val Thr Glu Asn Asn Asp Val Lys Ser
755 760 765

<210> 42

<211> 3168

<212> DNA

<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (1)..(3165)

<220>
<221> mat_peptide
<222> (144)..(3165)

<400> 42
atg ccc atg aag tgg agt ggg tgg agg tgg agc tgg ggg ccg gcc act 48
Met Pro Met Lys Trp Ser Gly Trp Arg Trp Ser Trp Gly Pro Ala Thr
-45 -40 -35

cac aca gcc ctc cca ccc cca cag ggt ttc tgc cgc agc gcc ctg cac 96
His Thr Ala Leu Pro Pro Pro Gln Gly Phe Cys Arg Ser Ala Leu His
-30 -25 -20

ccg ctg tct ctc ctg gtg cag gcc atc atg ctg gcc atg acc ctg gcc 144
Pro Leu Ser Leu Leu Val Gln Ala Ile Met Leu Ala Met Thr Leu Ala
15 -10 -5 -1

ctg ggt acc ttg cct gcc ttc cta ccc tgt gag ctc cag ccc cac ggc 192
Leu Gly Thr Leu Pro Ala Phe Leu Pro Cys Glu Leu Gln Pro His Gly
1 5 10 15

ctg gtg aac tgc aac tgg ctg ttc ctg aag tct gtg ccc cac ttc tcc 240
Leu Val Asn Cys Asn Trp Leu Phe Leu Lys Ser Val Pro His Phe Ser
20 25 30

atg gca gca ccc cgt ggc aat gtc acc agc ctt tcc ttg tcc tcc aac 288
Met Ala Ala Pro Arg Gly Asn Val Thr Ser Leu Ser Leu Ser Ser Asn
35 40 45

cgc atc cac cac ctc cat gat tct gac ttt gcc cac ctg ccc agc ctg 336
Arg Ile His His Leu His Asp Ser Asp Phe Ala His Leu Pro Ser Leu
50 55 60

cgg cat ctc aac ctc aag tgg aac tgc ccg ccg gtt ggc ctc agc ccc 384
Arg His Leu Asn Leu Lys Trp Asn Cys Pro Pro Val Gly Leu Ser Pro
65 70 75 80

atg cac ttc ccc tgc cac atg acc atc gag ccc agc acc ttc ttg gct 432
Met His Phe Pro Cys His Met Thr Ile Glu Pro Ser Thr Phe Leu Ala
85 90 95

gtg ccc acc ctg gaa gag cta aac ctg agc tac aac aac atc atg act 480
Val Pro Thr Leu Glu Glu Leu Asn Leu Ser Tyr Asn Asn Ile Met Thr
100 105 110

gtg cct gcg ctg ccc aaa tcc ctc ata tcc ctg tcc ctc agc cat acc 528

Val	Pro	Ala	Leu	Pro	Lys	Ser	Leu	Ile	Ser	Leu	Ser	Leu	Ser	His	Thr		
		115					120					125					
aac	atc	ctg	atg	cta	gac	tct	gcc	agc	ctc	gcc	ggc	ctg	cat	gcc	ctg	576	
Asn	Ile	Leu	Met	Leu	Asp	Ser	Ala	Ser	Leu	Ala	Gly	Leu	His	Ala	Leu		
	130					135					140						
cgc	ttc	cta	ttc	atg	gac	ggc	aac	tgt	tat	tac	aag	aac	ccc	tgc	agg	624	
Arg	Phe	Leu	Phe	Met	Asp	Gly	Asn	Cys	Tyr	Tyr	Lys	Asn	Pro	Cys	Arg		
145					150					155					160		
cag	gca	ctg	gag	gtg	gcc	ccg	ggc	gcc	ctc	ctt	ggc	ctg	ggc	aac	ctc	672	
Gln	Ala	Leu	Glu	Val	Ala	Pro	Gly	Ala	Leu	Leu	Gly	Leu	Gly	Asn	Leu		
				165					170					175			
acc	cac	ctg	tca	ctc	aag	tac	aac	aac	ctc	act	gtg	gtg	ccc	cgc	aac	720	
Thr	His	Leu	Ser	Leu	Lys	Tyr	Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Asn		
			180					185					190				
ctg	cct	tcc	agc	ctg	gag	tat	ctg	ctg	ttg	tcc	tac	aac	cgc	atc	gtc	768	
Leu	Pro	Ser	Ser	Leu	Glu	Tyr	Leu	Leu	Leu	Ser	Tyr	Asn	Arg	Ile	Val		
		195					200					205					
aaa	ctg	gcg	cct	gag	gac	ctg	gcc	aat	ctg	acc	gcc	ctg	cgt	gtg	ctc	816	
Lys	Leu	Ala	Pro	Glu	Asp	Leu	Ala	Asn	Leu	Thr	Ala	Leu	Arg	Val	Leu		
	210					215					220						
gat	gtg	ggc	gga	aat	tgc	cgc	cgc	tgc	gac	cac	gct	ccc	aac	ccc	tgc	864	
Asp	Val	Gly	Gly	Asn	Cys	Arg	Arg	Cys	Asp	His	Ala	Pro	Asn	Pro	Cys		
225					230					235					240		
atg	gag	tgc	cct	cgt	cac	ttc	ccc	cag	cta	cat	ccc	gat	acc	ttc	agc	912	
Met	Glu	Cys	Pro	Arg	His	Phe	Pro	Gln	Leu	His	Pro	Asp	Thr	Phe	Ser		
				245				250						255			
cac	ctg	agc	cgt	ctt	gaa	ggc	ctg	gtg	ttg	aag	gac	agt	tct	ctc	tcc	960	
His	Leu	Ser	Arg	Leu	Glu	Gly	Leu	Val	Leu	Lys	Asp	Ser	Ser	Leu	Ser		
			260					265					270				
tgg	ctg	aat	gcc	agt	tgg	ttc	cgt	ggg	ctg	gga	aac	ctc	cga	gtg	ctg	1008	
Trp	Leu	Asn	Ala	Ser	Trp	Phe	Arg	Gly	Leu	Gly	Asn	Leu	Arg	Val	Leu		
		275					280					285					
gac	ctg	agt	gag	aac	ttc	ctc	tac	aaa	tgc	atc	act	aaa	acc	aag	gcc	1056	
Asp	Leu	Ser	Glu	Asn	Phe	Leu	Tyr	Lys	Cys	Ile	Thr	Lys	Thr	Lys	Ala		
	290					295					300						
ttc	cag	ggc	cta	aca	cag	ctg	cgc	aag	ctt	aac	ctg	tcc	ttc	aat	tac	1104	
Phe	Gln	Gly	Leu	Thr	Gln	Leu	Arg	Lys	Leu	Asn	Leu	Ser	Phe	Asn	Tyr		
305					310					315					320		
caa	aag	agg	gtg	tcc	ttt	gcc	cac	ctg	tct	ctg	gcc	cct	tcc	ttc	ggg	1152	
Gln	Lys	Arg	Val	Ser	Phe	Ala	His	Leu	Ser	Leu	Ala	Pro	Ser	Phe	Gly		

325										330					335					
agc	ctg	gtc	gcc	ctg	aag	gag	ctg	gac	atg	cac	ggc	atc	ttc	ttc	cgc	1200				
Ser	Leu	Val	Ala	Leu	Lys	Glu	Leu	Asp	Met	His	Gly	Ile	Phe	Phe	Arg					
			340					345					350							
tca	ctc	gat	gag	acc	acg	ctc	cgg	cca	ctg	gcc	cgc	ctg	ccc	atg	ctc	1248				
Ser	Leu	Asp	Glu	Thr	Thr	Leu	Arg	Pro	Leu	Ala	Arg	Leu	Pro	Met	Leu					
		355					360					365								
cag	act	ctg	cgt	ctg	cag	atg	aac	ttc	atc	aac	cag	gcc	cag	ctc	ggc	1296				
Gln	Thr	Leu	Arg	Leu	Gln	Met	Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly					
	370					375					380									
atc	ttc	agg	gcc	ttc	cct	ggc	ctg	cgc	tac	gtg	gac	ctg	tcg	gac	aac	1344				
Ile	Phe	Arg	Ala	Phe	Pro	Gly	Leu	Arg	Tyr	Val	Asp	Leu	Ser	Asp	Asn					
385					390				395						400					
cgc	atc	agc	gga	gct	tcg	gag	ctg	aca	gcc	acc	atg	ggg	gag	gca	gat	1392				
Arg	Ile	Ser	Gly	Ala	Ser	Glu	Leu	Thr	Ala	Thr	Met	Gly	Glu	Ala	Asp					
				405					410					415						
gga	ggg	gag	aag	gtc	tgg	ctg	cag	cct	ggg	gac	ctt	gct	ccg	gcc	cca	1440				
Gly	Gly	Glu	Lys	Val	Trp	Leu	Gln	Pro	Gly	Asp	Leu	Ala	Pro	Ala	Pro					
			420					425					430							
gtg	gac	act	ccc	agc	tct	gaa	gac	ttc	agg	ccc	aac	tgc	agc	acc	ctc	1488				
Val	Asp	Thr	Pro	Ser	Ser	Glu	Asp	Phe	Arg	Pro	Asn	Cys	Ser	Thr	Leu					
		435					440					445								
aac	ttc	acc	ttg	gat	ctg	tca	cgg	aac	aac	ctg	gtg	acc	gtg	cag	ccg	1536				
Asn	Phe	Thr	Leu	Asp	Leu	Ser	Arg	Asn	Asn	Leu	Val	Thr	Val	Gln	Pro					
	450					455					460									
gag	atg	ttt	gcc	cag	ctc	tcg	cac	ctg	cag	tgc	ctg	cgc	ctg	agc	cac	1584				
Glu	Met	Phe	Ala	Gln	Leu	Ser	His	Leu	Gln	Cys	Leu	Arg	Leu	Ser	His					
465					470					475					480					
aac	tgc	atc	tcg	cag	gca	gtc	aat	ggc	tcc	cag	ttc	ctg	ccg	ctg	acc	1632				
Asn	Cys	Ile	Ser	Gln	Ala	Val	Asn	Gly	Ser	Gln	Phe	Leu	Pro	Leu	Thr					
				485					490					495						
ggt	ctg	cag	gtg	cta	gac	ctg	tcc	cac	aat	aag	ctg	gac	ctc	tac	cac	1680				
Gly	Leu	Gln	Val	Leu	Asp	Leu	Ser	His	Asn	Lys	Leu	Asp	Leu	Tyr	His					
			500					505					510							
gag	cac	tca	ttc	acg	gag	cta	cca	cga	ctg	gag	gcc	ctg	gac	ctc	agc	1728				
Glu	His	Ser	Phe	Thr	Glu	Leu	Pro	Arg	Leu	Glu	Ala	Leu	Asp	Leu	Ser					
		515					520				525									
tac	aac	agc	cag	ccc	ttt	ggc	atg	cag	ggc	gtg	ggc	cac	aac	ttc	agc	1776				
Tyr	Asn	Ser	Gln	Pro	Phe	Gly	Met	Gln	Gly	Val	Gly	His	Asn	Phe	Ser					
	530					535					540									

ctc	gtg	gct	cac	ctg	cgc	acc	ctg	cgc	cac	ctc	agc	ctg	gcc	cac	aac	1824
Phe	Val	Ala	His	Leu	Arg	Thr	Leu	Arg	His	Leu	Ser	Leu	Ala	His	Asn	
545					550					555					560	
aac	atc	cac	agc	caa	gtg	tcc	cag	cag	ctc	tgc	agt	acg	tcg	ctg	cgg	1872
Asn	Ile	His	Ser	Gln	Val	Ser	Gln	Gln	Leu	Cys	Ser	Thr	Ser	Leu	Arg	
				565					570					575		
gcc	ctg	gac	ttc	agc	ggc	aat	gca	ctg	ggc	cat	atg	tgg	gcc	gag	gga	1920
Ala	Leu	Asp	Phe	Ser	Gly	Asn	Ala	Leu	Gly	His	Met	Trp	Ala	Glu	Gly	
			580					585					590			
gac	ctc	tat	ctg	cac	ttc	ttc	caa	ggc	ctg	agc	ggg	ttg	atc	tgg	ctg	1968
Asp	Leu	Tyr	Leu	His	Phe	Phe	Gln	Gly	Leu	Ser	Gly	Leu	Ile	Trp	Leu	
		595					600					605				
gac	ttg	tcc	cag	aac	cgc	ctg	cac	acc	ctc	ctg	ccc	caa	acc	ctg	cgc	2016
Asp	Leu	Ser	Gln	Asn	Arg	Leu	His	Thr	Leu	Leu	Pro	Gln	Thr	Leu	Arg	
	610					615					620					
aac	ctc	ccc	aag	agc	cta	cag	gtg	ctg	cgt	ctc	cgt	gac	aat	tac	ctg	2064
Asn	Leu	Pro	Lys	Ser	Leu	Gln	Val	Leu	Arg	Leu	Arg	Asp	Asn	Tyr	Leu	
625					630					635					640	
gcc	ctc	ttt	aag	tgg	tgg	agc	ctc	cac	ttc	ctg	ccc	aaa	ctg	gaa	gtc	2112
Ala	Phe	Phe	Lys	Trp	Trp	Ser	Leu	His	Phe	Leu	Pro	Lys	Leu	Glu	Val	
				645					650					655		
ctc	gac	ctg	gca	gga	aac	cag	ctg	aag	gcc	ctg	acc	aat	ggc	agc	ctg	2160
Leu	Asp	Leu	Ala	Gly	Asn	Gln	Leu	Lys	Ala	Leu	Thr	Asn	Gly	Ser	Leu	
			660					665					670			
cct	gct	ggc	acc	cgg	ctc	cgg	agg	ctg	gat	gtc	agc	tgc	aac	agc	atc	2208
Pro	Ala	Gly	Thr	Arg	Leu	Arg	Arg	Leu	Asp	Val	Ser	Cys	Asn	Ser	Ile	
		675					680					685				
agc	ttc	gtg	gcc	ccc	ggc	ttc	ttt	tcc	aag	gcc	aag	gag	ctg	cga	gag	2256
Ser	Phe	Val	Ala	Pro	Gly	Phe	Phe	Ser	Lys	Ala	Lys	Glu	Leu	Arg	Glu	
	690					695					700					
ctc	aac	ctt	agc	gcc	aac	gcc	ctc	aag	aca	gtg	gac	cac	tcc	tgg	ttt	2304
Leu	Asn	Leu	Ser	Ala	Asn	Ala	Leu	Lys	Thr	Val	Asp	His	Ser	Trp	Phe	
705					710					715					720	
ggg	ccc	ctg	gcg	agt	gcc	ctg	caa	ata	cta	gat	gta	agc	gcc	aac	cct	2352
Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	Pro	
				725					730					735		
ctg	cac	tgc	gcc	tgt	ggg	gcg	gcc	ttt	atg	gac	ttc	ctg	ctg	gag	gtg	2400
Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	Val	
			740					745					750			
cag	gct	gcc	gtg	ccc	ggg	ctg	ccc	agc	cgg	gtg	aag	tgt	ggc	agt	ccg	2448

Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	Pro		
		755					760					765					
ggc	cag	ctc	cag	ggc	ctc	agc	atc	ttt	gca	cag	gac	ctg	cgc	ctc	tgc	2496	
Gly	Gln	Leu	Gln	Gly	Leu	Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	Cys		
	770					775					780						
ctg	gat	gag	gcc	ctc	tcc	tgg	gac	tgt	ttc	gcc	ctc	tcg	ctg	ctg	gct	2544	
Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	Ala		
785					790					795					800		
gtg	gct	ctg	ggc	ctg	ggc	gtg	ccc	atg	ctg	cat	cac	ctc	tgt	ggc	tgg	2592	
Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	Trp		
				805					810					815			
gac	ctc	tgg	tac	tgc	ttc	cac	ctg	tgc	ctg	gcc	tgg	ctt	ccc	tgg	cgg	2640	
Asp	Leu	Trp	Tyr	Cys	Phe	His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Trp	Arg		
			820					825					830				
ggg	cgg	caa	agt	ggg	cga	gat	gag	gat	gcc	ctg	ccc	tac	gat	gcc	ttc	2688	
Gly	Arg	Gln	Ser	Gly	Arg	Asp	Glu	Asp	Ala	Leu	Pro	Tyr	Asp	Ala	Phe		
		835					840					845					
gtg	gtc	ttc	gac	aaa	acg	cag	agc	gca	gtg	gca	gac	tgg	gtg	tac	aac	2736	
Val	Val	Phe	Asp	Lys	Thr	Gln	Ser	Ala	Val	Ala	Asp	Trp	Val	Tyr	Asn		
	850					855					860						
gag	ttt	cgg	ggg	cag	ctg	gag	gag	tgc	cgt	ggg	cgc	tgg	gca	ctc	cgc	2784	
Glu	Leu	Arg	Gly	Gln	Leu	Glu	Glu	Cys	Arg	Gly	Arg	Trp	Ala	Leu	Arg		
865					870					875					880		
ctg	tgc	ctg	gag	gaa	cgc	gac	tgg	ctg	cct	ggc	aaa	acc	ctc	ttt	gag	2832	
Leu	Cys	Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Lys	Thr	Leu	Phe	Glu		
				885					890					895			
aac	ctg	tgg	gcc	tcg	gtc	tat	ggc	agc	cgc	aag	acg	ctg	ttt	gtg	ctg	2880	
Asn	Leu	Trp	Ala	Ser	Val	Tyr	Gly	Ser	Arg	Lys	Thr	Leu	Phe	Val	Leu		
			900					905					910				
gcc	cac	acg	gac	cgg	gtc	agt	ggc	ctc	ttg	cgc	gcc	agc	ttc	ctg	ctg	2928	
Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu	Arg	Ala	Ser	Phe	Leu	Leu		
		915					920					925					
gcc	cag	cag	cgc	ctg	ctg	gag	gac	cgc	aag	gac	gtc	gtg	gtg	ctg	gtg	2976	
Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val		
	930					935					940						
atc	ctg	agc	cct	gac	ggc	cgc	cgc	tcc	cgc	tat	gtg	cgg	ctg	cgc	cag	3024	
Ile	Leu	Ser	Pro	Asp	Gly	Arg	Arg	Ser	Arg	Tyr	Val	Arg	Leu	Arg	Gln		
945					950					955					960		
cgc	ctc	tgc	cgc	cag	agt	gtc	ctc	ctc	tgg	ccc	cac	cag	ccc	agt	ggc	3072	
Arg	Leu	Cys	Arg	Gln	Ser	Val	Leu	Leu	Trp	Pro	His	Gln	Pro	Ser	Gly		
				965					970					975			

gag	cgc	agc	ttc	tgg	gcc	cag	ctg	ggc	atg	gcc	ctg	acc	agg	gac	aac	3120
gln	Arg	Ser	Phe	Trp	Ala	Gln	Leu	Gly	Met	Ala	Leu	Thr	Arg	Asp	Asn	
			980					985					990			

cac	cac	ttc	tat	aac	cgg	aac	ttc	tgc	cag	gga	ccc	acg	gcc	gaa	tag	3168
his	His	Phe	Tyr	Asn	Arg	Asn	Phe	Cys	Gln	Gly	Pro	Thr	Ala	Glu		
		995				1000					1005					

<210> 43
 <211> 1055
 <212> PRT
 <213> Unknown

<400> 43																
Met	Pro	Met	Lys	Trp	Ser	Gly	Trp	Arg	Trp	Ser	Trp	Gly	Pro	Ala	Thr	
			-45					-40					-35			
His	Thr	Ala	Leu	Pro	Pro	Pro	Gln	Gly	Phe	Cys	Arg	Ser	Ala	Leu	His	
		-30					-25					-20				
Pro	Leu	Ser	Leu	Leu	Val	Gln	Ala	Ile	Met	Leu	Ala	Met	Thr	Leu	Ala	
	15					-10					-5				-1	
Leu	Gly	Thr	Leu	Pro	Ala	Phe	Leu	Pro	Cys	Glu	Leu	Gln	Pro	His	Gly	
1				5					10					15		
Leu	Val	Asn	Cys	Asn	Trp	Leu	Phe	Leu	Lys	Ser	Val	Pro	His	Phe	Ser	
			20					25					30			
Met	Ala	Ala	Pro	Arg	Gly	Asn	Val	Thr	Ser	Leu	Ser	Leu	Ser	Ser	Asn	
		35					40					45				
Arg	Ile	His	His	Leu	His	Asp	Ser	Asp	Phe	Ala	His	Leu	Pro	Ser	Leu	
	50					55					60					
Arg	His	Leu	Asn	Leu	Lys	Trp	Asn	Cys	Pro	Pro	Val	Gly	Leu	Ser	Pro	
65					70				75						80	
Met	His	Phe	Pro	Cys	His	Met	Thr	Ile	Glu	Pro	Ser	Thr	Phe	Leu	Ala	
				85					90					95		
Val	Pro	Thr	Leu	Glu	Glu	Leu	Asn	Leu	Ser	Tyr	Asn	Asn	Ile	Met	Thr	
			100					105					110			
Val	Pro	Ala	Leu	Pro	Lys	Ser	Leu	Ile	Ser	Leu	Ser	Leu	Ser	His	Thr	
		115					120					125				
Asn	Ile	Leu	Met	Leu	Asp	Ser	Ala	Ser	Leu	Ala	Gly	Leu	His	Ala	Leu	
	130					135					140					
Arg	Phe	Leu	Phe	Met	Asp	Gly	Asn	Cys	Tyr	Tyr	Lys	Asn	Pro	Cys	Arg	

145		150		155		160									
Gln	Ala	Leu	Glu	Val	Ala	Pro	Gly	Ala	Leu	Leu	Gly	Leu	Gly	Asn	Leu
			165						170					175	
Thr	His	Leu	Ser	Leu	Lys	Tyr	Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Asn
			180					185					190		
Leu	Pro	Ser	Ser	Leu	Glu	Tyr	Leu	Leu	Leu	Ser	Tyr	Asn	Arg	Ile	Val
		195					200					205			
Lys	Leu	Ala	Pro	Glu	Asp	Leu	Ala	Asn	Leu	Thr	Ala	Leu	Arg	Val	Leu
	210					215					220				
Asp	Val	Gly	Gly	Asn	Cys	Arg	Arg	Cys	Asp	His	Ala	Pro	Asn	Pro	Cys
225					230					235					240
Met	Glu	Cys	Pro	Arg	His	Phe	Pro	Gln	Leu	His	Pro	Asp	Thr	Phe	Ser
				245					250					255	
His	Leu	Ser	Arg	Leu	Glu	Gly	Leu	Val	Leu	Lys	Asp	Ser	Ser	Leu	Ser
			260					265					270		
Trp	Leu	Asn	Ala	Ser	Trp	Phe	Arg	Gly	Leu	Gly	Asn	Leu	Arg	Val	Leu
		275					280					285			
Asp	Leu	Ser	Glu	Asn	Phe	Leu	Tyr	Lys	Cys	Ile	Thr	Lys	Thr	Lys	Ala
	290					295					300				
Phe	Gln	Gly	Leu	Thr	Gln	Leu	Arg	Lys	Leu	Asn	Leu	Ser	Phe	Asn	Tyr
305					310					315					320
Gln	Lys	Arg	Val	Ser	Phe	Ala	His	Leu	Ser	Leu	Ala	Pro	Ser	Phe	Gly
				325					330					335	
Ser	Leu	Val	Ala	Leu	Lys	Glu	Leu	Asp	Met	His	Gly	Ile	Phe	Phe	Arg
			340					345					350		
Ser	Leu	Asp	Glu	Thr	Thr	Leu	Arg	Pro	Leu	Ala	Arg	Leu	Pro	Met	Leu
		355					360					365			
Gln	Thr	Leu	Arg	Leu	Gln	Met	Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly
	370					375					380				
Ile	Phe	Arg	Ala	Phe	Pro	Gly	Leu	Arg	Tyr	Val	Asp	Leu	Ser	Asp	Asn
385					390					395					400
Arg	Ile	Ser	Gly	Ala	Ser	Glu	Leu	Thr	Ala	Thr	Met	Gly	Glu	Ala	Asp
				405					410					415	
Gly	Gly	Glu	Lys	Val	Trp	Leu	Gln	Pro	Gly	Asp	Leu	Ala	Pro	Ala	Pro
			420					425					430		
Val	Asp	Thr	Pro	Ser	Ser	Glu	Asp	Phe	Arg	Pro	Asn	Cys	Ser	Thr	Leu

435

440

445

Asn Phe Thr Leu Asp Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro
 450 455 460

Glu Met Phe Ala Gln Leu Ser His Leu Gln Cys Leu Arg Leu Ser His
 465 470 475 480

Asn Cys Ile Ser Gln Ala Val Asn Gly Ser Gln Phe Leu Pro Leu Thr
 485 490 495

Gly Leu Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His
 500 505 510

Glu His Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser
 515 520 525

Tyr Asn Ser Gln Pro Phe Gly Met Gln Gly Val Gly His Asn Phe Ser
 530 535 540

Phe Val Ala His Leu Arg Thr Leu Arg His Leu Ser Leu Ala His Asn
 545 550 555 560

Asn Ile His Ser Gln Val Ser Gln Gln Leu Cys Ser Thr Ser Leu Arg
 565 570 575

Ala Leu Asp Phe Ser Gly Asn Ala Leu Gly His Met Trp Ala Glu Gly
 580 585 590

Asp Leu Tyr Leu His Phe Phe Gln Gly Leu Ser Gly Leu Ile Trp Leu
 595 600 605

Asp Leu Ser Gln Asn Arg Leu His Thr Leu Leu Pro Gln Thr Leu Arg
 610 615 620

Asn Leu Pro Lys Ser Leu Gln Val Leu Arg Leu Arg Asp Asn Tyr Leu
 625 630 635 640

Ala Phe Phe Lys Trp Trp Ser Leu His Phe Leu Pro Lys Leu Glu Val
 645 650 655

Leu Asp Leu Ala Gly Asn Gln Leu Lys Ala Leu Thr Asn Gly Ser Leu
 660 665 670

Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser Ile
 675 680 685

Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg Glu
 690 695 700

Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp Phe
 705 710 715 720

Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	Pro	725	730	735
Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	Val	740	745	750
Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	Pro	755	760	765
Gly	Gln	Leu	Gln	Gly	Leu	Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	Cys	770	775	780
Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	Ala	785	790	795
Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	Trp	805	810	815
Asp	Leu	Trp	Tyr	Cys	Phe	His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Trp	Arg	820	825	830
Gly	Arg	Gln	Ser	Gly	Arg	Asp	Glu	Asp	Ala	Leu	Pro	Tyr	Asp	Ala	Phe	835	840	845
Val	Val	Phe	Asp	Lys	Thr	Gln	Ser	Ala	Val	Ala	Asp	Trp	Val	Tyr	Asn	850	855	860
Glu	Leu	Arg	Gly	Gln	Leu	Glu	Glu	Cys	Arg	Gly	Arg	Trp	Ala	Leu	Arg	865	870	875
Leu	Cys	Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Lys	Thr	Leu	Phe	Glu	885	890	895
Asn	Leu	Trp	Ala	Ser	Val	Tyr	Gly	Ser	Arg	Lys	Thr	Leu	Phe	Val	Leu	900	905	910
Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu	Arg	Ala	Ser	Phe	Leu	Leu	915	920	925
Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	930	935	940
Ile	Leu	Ser	Pro	Asp	Gly	Arg	Arg	Ser	Arg	Tyr	Val	Arg	Leu	Arg	Gln	945	950	955
Arg	Leu	Cys	Arg	Gln	Ser	Val	Leu	Leu	Trp	Pro	His	Gln	Pro	Ser	Gly	965	970	975
Gln	Arg	Ser	Phe	Trp	Ala	Gln	Leu	Gly	Met	Ala	Leu	Thr	Arg	Asp	Asn	980	985	990
His	His	Phe	Tyr	Asn	Arg	Asn	Phe	Cys	Gln	Gly	Pro	Thr	Ala	Glu		995	1000	1005

<210> 44
<211> 2289
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>
<221> CDS
<222> (1) .. (2079)

<400> 44
aac ctg tcc ttc aat tac cgc aag aag gta tcc ttt gcc cgc ctc cac 48
Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala Arg Leu His
1 5 10 15
ctg gca agt tcc ttt aag aac ctg gtg tca ctg cag gag ctg aac atg 96
Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu Leu Asn Met
20 25 30
aac ggc atc ttc ttc cgc ttg ctc aac aag tac acg ctc aga tgg ctg 144
Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Tyr Thr Leu Arg Trp Leu
35 40 45
gcc gat ctg ccc aaa ctc cac act ctg cat ctt caa atg aac ttc atc 192
Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met Asn Phe Ile
50 55 60
aac cag gca cag ctc agc atc ttt ggt acc ttc cga gcc ctt cgc ttt 240
Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala Leu Arg Phe
65 70 75 80
gtg gac ttg tca gac aat cgc atc agt ggg cct tca acg ctg tca gaa 288
Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr Leu Ser Glu
85 90 95
gcc acc cct gaa gag gca gat gat gca gag cag gag gag ctg ttg tct 336
Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu Leu Leu Ser
100 105 110
gcg gat cct cac cca gct ccg ctg agc acc cct gct tct aag aac ttc 384
Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser Lys Asn Phe
115 120 125
atg gac agg tgt aag aac ttc aag ttc aac atg gac ctg tct cgg aac 432
Met Asp Arg Cys Lys Asn Phe Lys Phe Asn Met Asp Leu Ser Arg Asn
130 135 140
aac ctg gtg act atc aca gca gag atg ttt gta aat ctc tca cgc ctc 480
Asn Leu Val Thr Ile Thr Ala Glu Met Phe Val Asn Leu Ser Arg Leu

145		150		155		160										
cag	tgt	ctt	agc	ctg	agc	cac	aac	tca	att	gca	cag	gct	gtc	aat	ggc	528
Gln	Cys	Leu	Ser	Leu	Ser	His	Asn	Ser	Ile	Ala	Gln	Ala	Val	Asn	Gly	
				165					170					175		
tct	cag	ttc	ctg	cgc	ctg	acc	ggg	ctg	cag	gtg	cta	gac	ctg	tcc	cac	576
Ser	Gln	Phe	Leu	Pro	Leu	Thr	Gly	Leu	Gln	Val	Leu	Asp	Leu	Ser	His	
			180					185					190			
aat	aag	ctg	gac	ctc	tac	cac	gag	cac	tca	ttc	acg	gag	cta	cca	cga	624
Asn	Lys	Leu	Asp	Leu	Tyr	His	Glu	His	Ser	Phe	Thr	Glu	Leu	Pro	Arg	
		195					200					205				
ctg	gag	gcc	ctg	gac	ctc	agc	tac	aac	agc	cag	ccc	ttt	agc	atg	aag	672
Leu	Glu	Ala	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	Gln	Pro	Phe	Ser	Met	Lys	
	210					215					220					
ggg	ata	ggc	cac	aat	ttc	agt	ttt	gtg	acc	cat	ctg	tcc	atg	cta	cag	720
Gly	Ile	Gly	His	Asn	Phe	Ser	Phe	Val	Thr	His	Leu	Ser	Met	Leu	Gln	
225					230				235						240	
agc	ctt	agc	ctg	gca	cac	aat	gac	att	cat	acc	cgt	gtg	tcc	tca	cat	768
Ser	Leu	Ser	Leu	Ala	His	Asn	Asp	Ile	His	Thr	Arg	Val	Ser	Ser	His	
				245					250					255		
ctc	aac	agc	aac	tca	gtg	agg	ttt	ctt	gac	ttc	agc	ggc	aac	ggg	atg	816
Leu	Asn	Ser	Asn	Ser	Val	Arg	Phe	Leu	Asp	Phe	Ser	Gly	Asn	Gly	Met	
			260					265					270			
ggc	cgc	atg	tgg	gat	gag	ggg	ggc	ctt	tat	ctc	cat	ttc	ttc	caa	ggc	864
Gly	Arg	Met	Trp	Asp	Glu	Gly	Gly	Leu	Tyr	Leu	His	Phe	Phe	Gln	Gly	
		275					280					285				
ctg	agt	ggc	gtg	ctg	aag	ctg	gac	ctg	tct	caa	aat	aac	ctg	cat	atc	912
Leu	Ser	Gly	Val	Leu	Lys	Leu	Asp	Leu	Ser	Gln	Asn	Asn	Leu	His	Ile	
	290					295					300					
ctc	cgg	ccc	cag	aac	ctt	gac	aac	ctc	ccc	aag	agc	ctg	aag	ctg	ctg	960
Leu	Arg	Pro	Gln	Asn	Leu	Asp	Asn	Leu	Pro	Lys	Ser	Leu	Lys	Leu	Leu	
	305				310					315					320	
agc	ctc	cga	gac	aac	tac	cta	tct	ttc	ttt	aac	tgg	acc	agt	ctg	tcc	1008
Ser	Leu	Arg	Asp	Asn	Tyr	Leu	Ser	Phe	Phe	Asn	Trp	Thr	Ser	Leu	Ser	
				325					330					335		
ttc	cta	ccc	aac	ctg	gaa	gtc	cta	gac	ctg	gca	ggc	aac	cag	cta	aag	1056
Phe	Leu	Pro	Asn	Leu	Glu	Val	Leu	Asp	Leu	Ala	Gly	Asn	Gln	Leu	Lys	
			340					345					350			
gcc	ctg	acc	aat	ggc	acc	ctg	cct	aat	ggc	acc	ctc	ctc	cag	aaa	ctc	1104
Ala	Leu	Thr	Asn	Gly	Thr	Leu	Pro	Asn	Gly	Thr	Leu	Leu	Gln	Lys	Leu	
		355					360					365				

gat Asp 370	gtc Val	agt Ser	agc Ser	aac Asn	agt Ser	atc Ile 375	gtc Val	tct Ser	gtg Val	gcc Ala	ccc Pro 380	ggc Gly	ttc Phe	ttt Phe	tcc Ser	1152
aag Lys 385	gcc Ala	aag Lys	gag Glu	ctg Leu	cga Arg 390	gag Glu	ctc Leu	aac Asn	ctt Leu	agc Ser 395	gcc Ala	aac Asn	gcc Ala	ctc Leu	aag Lys 400	1200
aca Thr	gtg Val	gac Asp	cac His	tcc Ser 405	tgg Trp	ttt Phe	ggg Gly	ccc Pro	att Ile 410	gtg Val	atg Met	aac Asn	ctg Leu	aca Thr 415	gtt Val	1248
cta Leu	gac Asp	gtg Val	aga Arg 420	agc Ser	aac Asn	cct Pro	ctg Leu	cac His	tgt Cys 425	gcc Ala	tgt Cys	ggg Gly	gca Ala 430	gcc Ala	tcc Phe	1296
gta Val	gac Asp	tta Leu 435	ctg Leu	ttg Leu	gag Glu	gtg Val	cag Gln 440	acc Thr	aag Lys	gtg Val	cct Pro	ggc Gly 445	ctg Leu	gct Ala	aat Asn	1344
ggg Gly 450	gtg Val	aag Lys	tgt Cys	ggc Gly	agc Ser	ccc Pro 455	ggc Gly	cag Gln	ctg Leu	cag Gln	ggc Gly 460	cgt Arg	agc Ser	atc Ile	ttc Phe	1392
gcg Ala 465	cag Gln	gac Asp	ctg Leu	cgg Arg 470	ctg Leu	tgc Cys	ctg Leu	gat Asp	gag Glu	gtc Val 475	ctc Leu	tct Ser	tgg Trp	gac Asp	tgc Cys 480	1440
ttt Phe	ggc Gly	ctt Leu	tca Ser 485	ctc Leu	ttg Leu	gct Ala	gtg Val	gcc Ala	gtg Val 490	ggc Gly	atg Met	gtg Val	gtg Val	cct Pro 495	ata Ile	1488
ctg Leu	cac His	cat His	ctc Leu 500	tgc Cys	ggc Gly	tgg Trp	gac Asp	gtc Val 505	tgg Trp	tac Tyr	tgt Cys	ttt Phe 510	cat His	ctg Leu	tgc Cys	1536
ctg Leu	gca Ala	tgg Trp 515	cta Leu	cct Pro	ttg Leu	cta Leu	gcc Ala 520	cgc Arg	agc Ser	cga Arg	cgc Arg	agc Ser 525	gcc Ala	caa Gln	act Thr	1584
ctc Leu 530	cct Pro	tat Tyr	gat Asp	gcc Ala	ttc Phe	gtg Val 535	gtg Val	ttc Phe	gat Asp	aag Lys	gca Ala 540	cag Gln	agc Ser	gca Ala	gtt Val	1632
gcc Ala 545	gac Asp	tgg Trp	gtg Val	tat Tyr	aac Asn 550	gag Glu	ctg Leu	cgg Arg	gtg Val	cgg Arg 555	ctg Leu	gag Glu	gag Glu	cgg Arg	cgc Arg 560	1680
ggc Gly	cgc Arg	tgg Trp	gca Ala	ctc Leu 565	cgc Arg	ctg Leu	tgc Cys	ctg Leu	gag Glu 570	gac Asp	cga Arg	gat Asp	tgg Trp	ctg Leu 575	cct Pro	1728
ggc Gly	cag Arg	acg Trp	ctc Leu	ttc Phe	gag Glu	aac Asn	ctc Leu	tgg Trp	gct Val	tcc Pro	atc Ile	tat Phe	ggg Gly	agc Ser	cgc Arg	1776

Gly	Gln	Thr	Leu	Phe	Glu	Asn	Leu	Trp	Ala	Ser	Ile	Tyr	Gly	Ser	Arg	
			580					585					590			
aag	act	cta	ttt	gtg	ctg	gcc	cac	acg	gac	cgc	gtc	agt	ggc	ctc	ctg	1824
Lys	Thr	Leu	Phe	Val	Leu	Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu	
		595					600					605				
cgc	acc	agc	ttc	ctg	ctg	gct	cag	cag	cgc	ctg	ttg	gaa	gac	cgc	aag	1872
Arg	Thr	Ser	Phe	Leu	Leu	Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys	
	610					615					620					
gac	gtg	gtg	gtg	ttg	gtg	atc	ctg	cgt	ccg	gat	gcc	cac	cgc	tcc	cgc	1920
Asp	Val	Val	Val	Leu	Val	Ile	Leu	Arg	Pro	Asp	Ala	His	Arg	Ser	Arg	
625					630					635					640	
tat	gtg	cga	ctg	cgc	cag	cgt	ctc	tgc	cgc	cag	agt	gtg	ctc	ttc	tgg	1968
Tyr	Val	Arg	Leu	Arg	Gln	Arg	Leu	Cys	Arg	Gln	Ser	Val	Leu	Phe	Trp	
				645					650					655		
ccc	cag	cag	ccc	aac	ggg	cag	ggg	ggc	ttc	tgg	gcc	cag	ctg	agt	aca	2016
Pro	Gln	Gln	Pro	Asn	Gly	Gln	Gly	Gly	Phe	Trp	Ala	Gln	Leu	Ser	Thr	
			660					665					670			
gcc	ctg	act	agg	gac	aac	cgc	cac	ttc	tat	aac	cag	aac	ttc	tgc	cgg	2064
Ala	Leu	Thr	Arg	Asp	Asn	Arg	His	Phe	Tyr	Asn	Gln	Asn	Phe	Cys	Arg	
		675					680					685				
gga	cct	aca	gca	gaa	tagctcagag	caacagctgg	aaacagctgc	atcttcatgt								2119
Gly	Pro	Thr	Ala	Glu												
ctg	ttcccg	agttgctctg	cctgccttgc	tctgtcttac	tacaccgcta	tttggcaagt										2179
gcg	aatata	tgctaccaag	ccaccaggcc	cacggagcaa	aggttggctg	taaagggtag										2239
ttttcttccc	atgcatcttt	caggagagtg	aagatagaca	ccaaaccac												2289

<210> 45
 <211> 693
 <212> PRT
 <213> Unknown

<400> 45
 Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala Arg Leu His
 1 5 10 15
 Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu Leu Asn Met
 20 25 30
 Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Tyr Thr Leu Arg Trp Leu
 35 40 45
 Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met Asn Phe Ile

50					55					60					
Asn	Gln	Ala	Gln	Leu	Ser	Ile	Phe	Gly	Thr	Phe	Arg	Ala	Leu	Arg	Phe
65					70					75					80
Val	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Ser	Gly	Pro	Ser	Thr	Leu	Ser	Glu
				85					90					95	
Ala	Thr	Pro	Glu	Glu	Ala	Asp	Asp	Ala	Glu	Gln	Glu	Glu	Leu	Leu	Ser
			100					105					110		
Ala	Asp	Pro	His	Pro	Ala	Pro	Leu	Ser	Thr	Pro	Ala	Ser	Lys	Asn	Phe
		115					120					125			
Met	Asp	Arg	Cys	Lys	Asn	Phe	Lys	Phe	Asn	Met	Asp	Leu	Ser	Arg	Asn
	130					135					140				
Asn	Leu	Val	Thr	Ile	Thr	Ala	Glu	Met	Phe	Val	Asn	Leu	Ser	Arg	Leu
145					150					155					160
Gln	Cys	Leu	Ser	Leu	Ser	His	Asn	Ser	Ile	Ala	Gln	Ala	Val	Asn	Gly
				165					170					175	
Ser	Gln	Phe	Leu	Pro	Leu	Thr	Gly	Leu	Gln	Val	Leu	Asp	Leu	Ser	His
			180					185					190		
Asn	Lys	Leu	Asp	Leu	Tyr	His	Glu	His	Ser	Phe	Thr	Glu	Leu	Pro	Arg
		195					200					205			
Leu	Glu	Ala	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	Gln	Pro	Phe	Ser	Met	Lys
						215					220				
Gly	Ile	Gly	His	Asn	Phe	Ser	Phe	Val	Thr	His	Leu	Ser	Met	Leu	Gln
225				230						235				240	
Ser	Leu	Ser	Leu	Ala	His	Asn	Asp	Ile	His	Thr	Arg	Val	Ser	Ser	His
				245					250					255	
Leu	Asn	Ser	Asn	Ser	Val	Arg	Phe	Leu	Asp	Phe	Ser	Gly	Asn	Gly	Met
			260					265					270		
Gly	Arg	Met	Trp	Asp	Glu	Gly	Gly	Leu	Tyr	Leu	His	Phe	Phe	Gln	Gly
		275					280					285			
Leu	Ser	Gly	Val	Leu	Lys	Leu	Asp	Leu	Ser	Gln	Asn	Asn	Leu	His	Ile
						295					300				
Leu	Arg	Pro	Gln	Asn	Leu	Asp	Asn	Leu	Pro	Lys	Ser	Leu	Lys	Leu	Leu
305				310						315				320	
Ser	Leu	Arg	Asp	Asn	Tyr	Leu	Ser	Phe	Phe	Asn	Trp	Thr	Ser	Leu	Ser
				325					330					335	

he Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn Gln Leu Lys
 340 345 350
 la Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu Gln Lys Leu
 355 360 365
 sp Val Ser Ser Asn Ser Ile Val Ser Val Ala Pro Gly Phe Phe Ser
 370 375 380
 ys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 85 390 395 400
 thr Val Asp His Ser Trp Phe Gly Pro Ile Val Met Asn Leu Thr Val
 405 410 415
 leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 420 425 430
 val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly Leu Ala Asn
 435 440 445
 Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 450 455 460
 Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser Trp Asp Cys
 465 470 475 480
 Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val Val Pro Ile
 485 490 495
 Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe His Leu Cys
 500 505 510
 Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser Ala Gln Thr
 515 520 525
 Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val
 530 535 540
 Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg Arg
 545 550 555 560
 Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp Trp Leu Pro
 565 570 575
 Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr Gly Ser Arg
 580 585 590
 Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu
 595 600 605
 Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys
 610 615 620

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser Arg
625 630 635 640

Yr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe Trp
645 650 655

Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln Leu Ser Thr
660 665 670

Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe Cys Arg
675 680 685

Gly Pro Thr Ala Glu
690

Variable	Mean	SD	Min	Max
Age	38.5	10.5	25	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	15.5	5.5	10	25
Health status	1.5	0.5	1	2
Stress level	2.5	1.5	1	4
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.5	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.5	1.5	1	5
Overall satisfaction	3.5	1.5	1	5



UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, D.C. 20231
www.uspto.gov

APPLICATION NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTY. DOCKET NO./TITLE
09/728,540	11/28/2000	Gerard T. Hardiman	DX0724XK

28008
DNAX RESEARCH INSTITUTE
LEGAL DEPARTMENT
901 CALIFORNIA AVENUE
PALO ALTO, CA 94304

CONFIRMATION NO. 4490

CORRECTION COVER LETTER



OC000000006158481

Date Mailed: 06/07/2001

COVER LETTER FOR CORRECTION OF PREVIOUS NOTICE

The Notice mailed on 02/08/2001 was sent in error and is hereby withdrawn. A corrected Notice is enclosed.
The time period for reply runs from the mail date of the corrected Notice. We apologize for any inconvenience this caused.

FOOT 60" T-400564

A copy of this notice MUST be returned with the reply.

Customer Service Center
Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE



UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, D.C. 20231
www.uspto.gov

APPLICATION NUMBER	FILING RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/728,540	11/28/2000	Gerard T. Hardiman	DX0724XK

28008
DNAX RESEARCH INSTITUTE
LEGAL DEPARTMENT
901 CALIFORNIA AVENUE
PALO ALTO, CA 94304

CONFIRMATION NO. 4490

FORMALITIES LETTER



OC000000006158487

Date Mailed: 06/07/2001

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given TWO MONTHS FROM THE DATE OF THIS NOTICE within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- This application does not contain a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d). Applicant must provide such statement. If the effective filing date is on or after September 8, 2000, see the final rulemaking notice published in the Federal Register at 65 FR 54604 (September 8, 2000) and 1238 OG 145 (September 19, 2000).
- A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e). If the effective filing date is on or after September 8, 2000, see the final rulemaking notice published in the Federal Register at 65 FR 54604 (September 8, 2000) and 1238 OG 145 (September 19, 2000). Applicant must provide an initial computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d). If applicant desires the sequence listing in the instant application to be identical with that of another application on file in the U.S. Patent and Trademark Office, such request in accordance with 37 CFR 1.821(e) may be submitted in lieu of a new CRF.

For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

